

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 04:08:08 ; Search time 1358.3 Seconds

(without alignments)
16712.222 Million cell updates/sec

Title: US-09-869-894-1

Perfect score: 780

Sequence: 1 gaatgagcatctcagcaca.....aatgtatgtatttctt 780

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: listing first 45 Summaries

Database :

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41: em_hlgo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	28	3.6	28	6 AR091102	AR091102 Sequence
C 2	28	3.6	28	6 AR198137	AR198137 Sequence
C 3	26	3.3	26	6 AR091101	AR091101 Sequence
C 4	25	3.3	26	6 AR198136	AR198136 Sequence
C 5	22	2.8	22	6 AR095064	AR095064 Sequence
C 6	20	2.6	20	6 AR095049	AR095049 Sequence
C 7	20	2.6	20	6 AR095050	AR095050 Sequence
C 8	20	2.6	20	6 AR095051	AR095051 Sequence
C 9	20	2.6	20	6 AR095052	AR095052 Sequence
C 10	20	2.6	20	6 AR095053	AR095053 Sequence
C 11	20	2.6	20	6 AR095054	AR095054 Sequence
C 12	20	2.6	20	6 AR095055	AR095055 Sequence
C 13	20	2.6	20	6 AR095056	AR095056 Sequence
C 14	20	2.6	20	6 AR095057	AR095057 Sequence
C 15	20	2.6	20	6 AR095058	AR095058 Sequence
C 16	20	2.6	20	6 AR095059	AR095059 Sequence
C 17	20	2.6	20	6 AR095060	AR095060 Sequence
C 18	20	2.6	20	6 AR095061	AR095061 Sequence
C 19	20	2.6	20	6 AR095062	AR095062 Sequence
C 20	20	2.6	20	6 AR095063	AR095063 Sequence
C 21	16	2.1	16	6 A22329	A22329 Sequence
C 22	15	2.1	15	6 A22330	A22330 Sequence
C 23	15	1.9	15	6 AX236036	AX236036 Sequence
C 24	14	1.8	14	6 AX132760	AX132760 Sequence
C 25	14	1.8	14	6 AX132761	AX132761 Sequence
C 26	14	1.8	14	6 AX132762	AX132762 Sequence
C 27	14	1.8	14	6 AX132763	AX132763 Sequence
C 28	14	1.8	14	6 AX132764	AX132764 Sequence
C 29	14	1.8	14	6 AX008457	AX008457 Sequence
C 30	14	1.8	14	6 AX020687	AX020687 Sequence
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C 33	14	1.8	14	6 AX045385	AX045385 Sequence
C 34	14	1.8	14	6 AX045389	AX045389 Sequence
C 35	14	1.8	14	6 AX482149	AX482149 Sequence
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C 37	14	1.8	14	6 AR069502	AR069502 Sequence
C 38	14	1.8	14	6 AR195122	AR195122 Sequence
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C 40	14	1.8	14	6 AX469912	AX469912 Sequence
C 41	14	1.8	14	6 AR070762	AR070762 Sequence
C 42	14	1.8	14	6 AR122968	AR122968 Sequence
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C 44	14	1.8	14	6 AX059211	AX059211 Sequence
C 45	14	1.8	14	6 I28164	I28164 Sequence
C 46	14	1.8	14	6 AX474377	AX474377 Sequence

ALIGNMENTS

RESULT 1
AR091102/c
LOCUS AR091102 28 bp DNA
DEFINITION Sequence 1222 from patent US 594076.
ACCESSION AR091102
VERSION AR091102.1 GI:10017857
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik, A., Jorhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 594076-A 1222 30-NOV-1999;
FEATURES Location/Qualifiers

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BASE COUNT 6 a 4 c 9 g 9 t
ORIGIN

Query Match
Best Local Similarity 3.6%; Score 28; DB 6; Length 28;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 TCCGTAGACACTGCAGAACACTATCA 292
DB 28 TCCGTAGACACTGCAGAACACTATCA 1

RESULT 2
ARI98137/c
LOCUS ARI98137 28 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1222 from patent US 6352829.
ACCESSION ARI98137
VERSION ARI98137.1 GI:20247986
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jorhadze,G. and Bibilashvili,I.R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 1222 05-MAR-2002;
FEATURES
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/organism="unknown"
BASE COUNT 6 a 4 c 9 g 9 t
ORIGIN

Query Match
Best Local Similarity 3.6%; Score 28; DB 6; Length 28;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 TCCGTAGACACTGCAGAACACTATCA 292
DB 28 TCCGTAGACACTGCAGAACACTATCA 1

RESULT 3
AR091101
LOCUS AR091101 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1221 from patent US 5994076.
ACCESSION AR091101
VERSION AR091101.1 GI:10017856
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jorhadze,G. and Bibilashvili,I.R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 1221 30-NOV-1999;
FEATURES
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1. .26
/organism="unknown"
BASE COUNT 9 a 7 c 7 g 3 t
ORIGIN

Query Match
Best Local Similarity 3.3%; Score 26; DB 6; Length 26;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 TCCACCAGCAGAGATGACAGACTG 89
DB 1 TCCACCAGCAGAGATGACAGACTG 26

RESULT 4

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ARI98136
LOCUS ARI98136 26 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1221 from patent US 6352829.
ACCESSION ARI98136
VERSION ARI98136.1 GI:20247985
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jorhadze,G. and Bibilashvili,I.R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 1221 05-MAR-2002;
FEATURES
source
1. .26
/organism="unknown"
BASE COUNT 9 a 7 c 7 g 3 t
ORIGIN

Query Match
Best Local Similarity 3.3%; Score 26; DB 6; Length 26;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 TCCACCAGCAGAGATGACAGACTG 89
DB 1 TCCACCAGCAGAGATGACAGACTG 26

RESULT 5
AR095064/c
LOCUS AR095064 22 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 17 from patent US 6001992.
ACCESSION AR095064
VERSION AR095064.1 GI:10022579
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Ackermann,E.J., Bennett,C.,Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 17 14-DEC-1999;
FEATURES
source
1. .22
/organism="unknown"
BASE COUNT 6 a 2 c 7 g 7 t
ORIGIN

Query Match
Best Local Similarity 2.8%; Score 22; DB 6; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 ACGATTGCCAACACATCTTCT 684
DB 22 ACGATTGCCAACACATCTTCT 1

RESULT 6
AR095049/c
LOCUS AR095049 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 2 from patent US 6001992.
ACCESSION AR095049
VERSION AR095049.1 GI:10022549
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.,Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 2 14-DEC-1999;
FEATURES
source
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BASE COUNT      5 a      6 c      6 g      3 t
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Query Match      2.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 GCGGCTCAGACATCTGTC 130
Db 20 GCTGCTCAGACATCTGTC 1

RESULT 12
LOCUS AR095055/c 20 bp DNA Linear PAT 08-SEP-2000
DEFINITION Sequence 8 from patent US 6001992.
ACCESSION AR095055
VERSION AR095055.1 GI:10022561
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 8 14-DEC-1999;
FEATURES
Source 1..20
Location/Qualifiers
/organism="unknown"

BASE COUNT      7 a      4 c      5 g      4 t
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Best Local Similarity 100.0%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 AATGTTGGCTCTCAGTCCA 212
Db 20 AATGTTGGCTCTCAGTCCA 1

RESULT 13
LOCUS AR095056/c 20 bp DNA Linear PAT 08-SEP-2000
DEFINITION Sequence 9 from patent US 6001992.
ACCESSION AR095056
VERSION AR095056.1 GI:10022563
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 9 14-DEC-1999;
FEATURES
Source 1..20
Location/Qualifiers
/organism="unknown"

BASE COUNT      4 a      3 c      6 g      7 t
ORIGIN
Query Match      2.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GACACTGCAGACACTATT 290
Db 20 GACACTGCAGACACTATT 1

RESULT 14
LOCUS AR095057/c 20 bp DNA Linear PAT 08-SEP-2000

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DEFINITION Sequence 10 from patent US 6001992.
ACCESSION AR095057
VERSION AR095057.1 GI:10022565
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 10 14-DEC-1999;
FEATURES
Source 1..20
Location/Qualifiers
/organism="unknown"

BASE COUNT      4 a      7 c      3 g      6 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 GGACTTTGAAGACGGCATCA 328
Db 20 GGACTTTGAAGACGGCATCA 1

RESULT 15
LOCUS AR095058/c 20 bp DNA Linear PAT 08-SEP-2000
DEFINITION Sequence 11 from patent US 6001992.
ACCESSION AR095058
VERSION AR095058.1 GI:10022567
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 11 14-DEC-1999;
FEATURES
Source 1..20
Location/Qualifiers
/organism="unknown"

BASE COUNT      3 a      3 c      5 g      9 t
ORIGIN
Query Match      2.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 AAGAACTTCTACGACACCA 398
Db 20 AAGAACTTCTACGACACCA 1

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Search completed: March 14, 2003, 07:13:17
 Job time : 1363.8 secs

Matches 28: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 265 TCCGTAGACACTGCCAGAACTATCA 292

Db 28 TCCGTAGACACTGCCAGAACTATCA 1

RESULT 2

US-09-225-928-1222/c

Sequence 1222, Application US/09225928

Patent No. 6352829

GENERAL INFORMATION:

APPLICANT: Chenchik, Alex

Jokhadze, George

Biblashvili, Robert

TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

NUMBER OF SEQUENCES: 1375

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park

STATE: CA

COUNTRY: US

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/225,928

FILING DATE: 05-Jan-1999

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/859,998

FILING DATE: 21-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Field, Bret E.

REGISTRATION NUMBER: 37,620

REFERENCE/DOCKET NUMBER: 09096/002001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070

TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 1222:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

OTHER INFORMATION: oligonucleotide primer

SEQUENCE DESCRIPTION: SEQ ID NO: 1222:

US-09-225-928-1222

Query Match 3.6%; Score 28; DB 4; Length 28;

Best Local Similarity 100.0%; Pred. No. 7.2e-05;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 265 TCCGTAGACACTGCCAGAACTATCA 292

Db 28 TCCGTAGACACTGCCAGAACTATCA 1

RESULT 3

US-08-859-998-1221

Sequence 1221, Application US/08859998

Patent No. 5994076

GENERAL INFORMATION:

APPLICANT: Chenchik, Alex

Jokhadze, George

APPLICANT: Biblashvili, Robert

TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

NUMBER OF SEQUENCES: 1375

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park

STATE: CA

COUNTRY: US

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/859,998

FILING DATE: 21-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Field, Bret E.

REGISTRATION NUMBER: 37,620

REFERENCE/DOCKET NUMBER: 09096/002001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070

TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 1221:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

OTHER INFORMATION: oligonucleotide primer

US-08-859-998-1221

Query Match 3.3%; Score 26; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.00075;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 TCCACGACGACGAGATGACAGACTG 89

Db 1 TCCACGACGACGAGATGACAGACTG 26

RESULT 4

US-09-225-928-1221

Sequence 1221, Application US/09225928

Patent No. 6352829

GENERAL INFORMATION:

APPLICANT: Chenchik, Alex

Jokhadze, George

Biblashvili, Robert

TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

NUMBER OF SEQUENCES: 1375

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park

STATE: CA

COUNTRY: US

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:


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; TITLE OF INVENTION: bcl-2-Related Proteins
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-226-568-4

Query Match
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 GGTGAGCCAGCTCAGACTT 58
DB 20 GGTGAGCCAGCTCAGACTT 1

RESULT 9
US-09-226-568-5/c
; Sequence 5, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-226-568-5

Query Match
Best Local Similarity 100.0%; Pred. No. 0.85; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 CACCAAGCAGAGATGACAG 85
DB 20 CACCAAGCAGAGATGACAG 1

RESULT 10
US-09-226-568-6/c
; Sequence 6, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-226-568-6
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; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-226-568-6

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Best Local Similarity 100.0%; Pred. No. 0.85; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 GAATTGGATATATTACAG 110
DB 20 GAATTGGATATATTACAG 1

RESULT 11
US-09-226-568-7/c
; Sequence 7, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-226-568-7

Query Match
Best Local Similarity 100.0%; Pred. No. 0.85; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 GCTGCTCAGACTATCTGC 130
DB 20 GCTGCTCAGACTATCTGC 1

RESULT 12
US-09-226-568-8/c
; Sequence 8, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
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US-09-226-568-8
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence
US-09-226-568-8

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Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 AATGTCGCTCTCAGTCCA 212
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DB 20 AATGTCGCTCTCAGTCCA 1

RESULT 13
US-09-226-568-9/c
Sequence 9, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence
US-09-226-568-9

Query Match 2.6%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GACACTGCAGACACTATT 290
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DB 20 GACACTGCAGACACTATT 1

RESULT 14
US-09-226-568-10/c
Sequence 10, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence
US-09-226-568-10

Query Match 2.6%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 GGAGTTTGAGACGGCATCA 328
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DB 20 GGAGTTTGAGACGGCATCA 1

RESULT 15
US-09-226-568-11/c
Sequence 11, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence
US-09-226-568-11

Query Match 2.6%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 AAGAACTTCTACGACAGCA 398
|||||
DB 20 AAGAACTTCTACGACAGCA 1

Search completed: March 14, 2003, 08:31:49
Job time : 21.863 secs

GenCore version 5.1.4-ps_4578
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 07:14:05 ; Search time 49.143 Seconds
(without alignments)
11140.041 Million cell updates/sec

Title: US-09-869-894-1
Perfect score: 780
Sequence: 1 gagtggacattctcagcaca.....aattgtatgtattttctct 780

Scoring table: OLIGO_NMC
Gapop 60.0 , Gapext 60.0

Searched: 501302 seqs, 350932545 residues

Word size : 0

Total number of hits satisfying chosen parameters: 282380

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14	1.8	20	9	US-09-834-721-6
C 2	14	1.8	20	9	US-09-854-883-248
C 3	14	1.8	20	10	US-09-752-639-24
C 4	14	1.8	20	10	US-09-984-198-24
C 5	14	1.8	20	10	US-09-951-536-6
C 6	14	1.8	20	10	US-09-963-521-6
C 7	14	1.8	25	10	US-09-396-399-34
C 8	14	1.8	25	10	US-09-899-361-34
C 9	14	1.8	27	9	US-10-083-168-57
C 10	14	1.8	27	10	US-09-804-690-17
C 11	14	1.8	30	9	US-10-092-140-4
C 12	13	1.7	19	9	US-09-909-567B-35
C 13	13	1.7	20	9	US-09-734-672-60
C 14	13	1.7	20	9	US-09-982-828-60
C 15	13	1.7	20	9	US-10-022-819-55
C 16	13	1.7	20	10	US-09-800-631-81
C 17	13	1.7	20	10	US-09-800-631-82
C 18	13	1.7	21	9	US-09-692-396-44
C 19	13	1.7	23	9	US-09-944-413-20

C 20	13	1.7	23	9	US-09-944-403-20	Sequence 20, Appl
C 21	13	1.7	23	9	US-09-944-896-20	Sequence 20, Appl
C 22	13	1.7	23	9	US-09-944-944-20	Sequence 20, Appl
C 23	13	1.7	23	9	US-09-944-907-20	Sequence 20, Appl
C 24	13	1.7	23	9	US-09-944-929-20	Sequence 20, Appl
C 25	13	1.7	23	9	US-10-024-018-1	Sequence 1, Appl1
C 26	13	1.7	23	10	US-09-841-366A-58	Sequence 58, Appl
C 27	13	1.7	23	10	US-09-866-028-20	Sequence 20, Appl
C 28	13	1.7	23	10	US-09-944-449-20	Sequence 20, Appl
C 29	13	1.7	23	10	US-09-944-557-20	Sequence 20, Appl
C 30	13	1.7	23	10	US-09-945-587-20	Sequence 20, Appl
C 31	13	1.7	23	10	US-09-945-015-20	Sequence 20, Appl
C 32	13	1.7	23	10	US-09-944-396-20	Sequence 20, Appl
C 33	13	1.7	23	10	US-09-944-097-20	Sequence 20, Appl
C 34	13	1.7	23	10	US-09-944-433-20	Sequence 20, Appl
C 35	13	1.7	23	10	US-09-944-762-20	Sequence 20, Appl
C 36	13	1.7	23	10	US-09-944-654-20	Sequence 20, Appl
C 37	13	1.7	23	10	US-09-943-851A-20	Sequence 20, Appl
C 38	13	1.7	24	9	US-10-167-528-2	Sequence 2, Appl1
C 39	13	1.7	24	10	US-09-860-793-16	Sequence 16, Appl
C 40	13	1.7	31	10	US-09-782-650-18	Sequence 18, Appl
C 41	13	1.7	31	10	US-09-782-650-19	Sequence 19, Appl
C 42	13	1.7	32	10	US-09-930-251-9	Sequence 9, Appl1
C 43	13	1.7	42	9	US-10-206-654-1	Sequence 359, App
C 44	13	1.7	45	9	US-09-747-377-359	Sequence 192, App
C 45	13	1.7	50	9	US-09-992-598-192	

ALIGNMENTS

RESULT 1
US-09-834-721-6/c
; Sequence 6, Application US/09834721
; Patent No. US2002015551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Primer
US-09-834-721-6
Query Match 1.8%; Score 14; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 472 GAATGATTAAGCA 485
DB 17 GAATGATTAAGCA 4

RESULT 2
US-09-854-883-248/c
; Sequence 248, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freiler

APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
FILE REFERENCE: ISPH-0576
CURRENT APPLICATION NUMBER: US/09/854,883
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/629,644
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
SEQ ID NO 248
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-248

Query Match 1.8%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 GATGGAAGAAGAGT 313
DB 14 GATGGAAGAAGAGT 1

RESULT 3
US-09-752-639-24/C
Sequence 24, Application US/09752639
Patent No. US20020091243A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Gatanaga, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: Of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,639
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
FILING DATE:
APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-752-639-24

Query Match 1.8%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 GATTGTACCATA 354
DB 20 GATTGTACCATA 7

RESULT 4
US-09-984-198-24/C
Sequence 24, Application US/09984198
Patent No. US20020106679A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Gatanaga, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: Of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,198
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
FILING DATE:
APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-984-198-24

Query Match 1.8%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 341 GAATGTATACCAT 354
|||||
DB 20 GAATGTATACCAT 7

RESULT 5
US-09-951-536-6/c

Sequence 6, Application US/09951536
Patent No. US20020107378A1
GENERAL INFORMATION:
APPLICANT: ZIEGLER, PETRA
APPLICANT: ZIEGLER, LOTMAR
APPLICANT: SAHM, HERMANN
APPLICANT: THIREBACH, GEORG
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE AND
TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
TITLE OF INVENTION: USING CORNEFORM BACTERIA
FILE REFERENCE: 21123/282414/MAS
CURRENT FILING DATE: 2001-09-14
PRIORITY FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-951-536-6

Query Match 1.8%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 472 GAATGATAGGCA 485
|||||
DB 17 GAATGATAGGCA 4

RESULT 6
US-09-963-521-6/c

Sequence 6, Application US/09963521
Patent No. US20020146781A1
GENERAL INFORMATION:
APPLICANT: ZIEGLER, PETRA
APPLICANT: ZIEGLER, LOTMAR
APPLICANT: SAHM, HERMANN
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THREE GENE
TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
TITLE OF INVENTION: L-THREONINE USING CORNEFORM BACTERIA
FILE REFERENCE: 21123/282413/MAS
CURRENT FILING DATE: 2001-09-27
PRIORITY FILING DATE: 1999-11-01
PRIORITY FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-963-521-6

Query Match 1.8%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 472 GAATGATAGGCA 485
|||||
DB 17 GAATGATAGGCA 4

RESULT 7
US-09-398-399-34

Sequence 34, Application US/09398399
Patent No. US20020051973A1
GENERAL INFORMATION:
APPLICANT: DELENSTARR, GLENDA C.
APPLICANT: LEFKOWITZ, STEVEN M.
APPLICANT: LOEBKE, KEVIN J.
APPLICANT: OVERMAN, LESLIE B.
APPLICANT: SAMPRAS, NICHOLAS M.
APPLICANT: SAMPSON, JEFFREY R.
APPLICANT: WOLBER, PAUL K.
TITLE OF INVENTION: TECHNIQUES FOR ASSESSING NONSPECIFIC BINDING OF NUCLEIC
TITLE OF INVENTION: ACIDS TO SURFACES
FILE REFERENCE: 10981620-1
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-398-399-34

Query Match 1.8%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 531 ATCTGGCTGATGA 544
|||||
DB 12 ATCTGGCTGATGA 25

RESULT 8
US-09-899-381-34

Sequence 34, Application US/09899381
Patent No. US20020068293A1
GENERAL INFORMATION:
APPLICANT: Delenstarr, Glend C.
APPLICANT: Wolber, Paul K.
TITLE OF INVENTION: Arrays Having Background Features and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: 10010760-1
CURRENT FILING DATE: 2001-07-05
PRIORITY FILING DATE: 1999-09-17
PRIORITY FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic probe
US-09-899-381-34

Query Match 1.8%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 531 ATCTGGCTGATGA 544
|||||
DB 12 ATCTGGCTGATGA 25

RESULT 9
US-10-083-168-57
; Sequence 57, Application US/10083168
; Publication No. US20030023069A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Maciejewski-Lentor, Dominique
; APPLICANT: Leonard, James N.
; APPLICANT: Ortuno, Daniel
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
; FILE REFERENCE: AREN-0320
; CURRENT APPLICATION NUMBER: US/10/083,168
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 57
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: No. US20030023069A1ei Sequence
US-10-083-168-57
Query Match 1.8%; Score 14; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 42 GAGCCAGCTCAAGA 55
Db 3 GAGCCAGCTCAAGA 16
RESULT 10
US-09-804-690-17
; Sequence 17, Application US/09804690
; Patent No. US20020034743A1
; GENERAL INFORMATION:
; APPLICANT: LI, Lamin
; COHEN, Stanley N
; TITLE OF INVENTION: MAMMALIAN TUMOR SUSCEPTIBILITY GENES AND
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH AND RICHARDSON, P.C.
; STREET: 2200 SAND HILL ROAD
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/804,690
; FILING DATE: 12-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/146,187
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SHEPMOD, Pamela J
; REGISTRATION NUMBER: 36,677
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249

TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-804-690-17
Query Match 1.8%; Score 14; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 42 GAGCCAGCTCAAGA 55
Db 12 GAGCCAGCTCAAGA 25
RESULT 11
US-10-092-140-4
; Sequence 4, Application US/10092140
; Patent No. US20020164801A1
; GENERAL INFORMATION:
; APPLICANT: McGill University et al.
; TITLE OF INVENTION: HUMAN AND MAMMALIAN DNA
; REPLICATION ORIGIN CONSENSUS SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SWABY OGILVY RENAULT
; STREET: 1981 McGill College Avenue - Suite 1600
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/092,140
; FILING DATE: 06-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,750
; FILING DATE: 09-Jun-1999
; APPLICATION NUMBER: 60/033,374
; FILING DATE: 16-DEC-1996
; APPLICATION NUMBER: 60/047,322
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cst, France
; REGISTRATION NUMBER: 4166
; REFERENCE/DOCKET NUMBER: 1770-162PCT FC/1d
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514 845-7126
; TELEFAX: 514 288-8389
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-092-140-4
Query Match 1.8%; Score 14; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 431 TTTTCATTTTGT 444

Db 8 TTTTCATTTTGT 21

RESULT 12

US-09-909-567B-35
; Sequence 35, Application US/0909567B
; Publication No. US2003002257A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto A.
; APPLICANT: Nair, Manoj
; APPLICANT: Chen, Seiyu
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DEX-0214
; CURRENT APPLICATION NUMBER: US/09/909,567B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,834
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ. ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ. ID NO 35
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-909-567B-35

Query Match 1.7%; Score 13; DB 9; Length 19;

Best Local Similarity 100.0%; Pred. No. 6,1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 535 GCGTGATGACTT 547

Db 3 GCGTGATGACTT 15

RESULT 13

US-09-734-672-60/c
; Sequence 60, Application US/09734672
; Publication No. US20020183268A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; Allen, Antonette C.
; Alvares, Christopher P.
; Ciltz, Brenda S.
; Olson, Sheri J.
; Schelter, Denise B.
; Zeng, Bin

TITLE OF INVENTION: Coding Sequences of the Human

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Ave., N.W.
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 03-Dec-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/966,436
FILING DATE: 07-No. US20020183268A1-97

APPLICATION NUMBER: US 08/598,591

FILING DATE: 12-Feb-96

ATTORNEY/AGENT INFORMATION:

NAME: Michael S. Tuscan

REGISTRATION NUMBER: 43,210

REFERENCE/DOCKET NUMBER: 44921-5055-02-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-739-3000

TELEFAX: 202-739-3001

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: No. US20020183268A1 Relevant

MOLECULE TYPE: DNA (genomic)

TOPOLOGY: linear

ORIGINAL SOURCE:

STRAIN: 18R primer

SEQUENCE DESCRIPTION: SEQ ID NO: 60:

US-09-734-672-60

Query Match 1.7%; Score 13; DB 9; Length 20;

Best Local Similarity 100.0%; Pred. No. 6,2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 494 GCTGGGAATG 506

Db 17 GCTGGGAATG 5

RESULT 14

US-09-982-828-60/c
; Sequence 60, Application US/09982828
; Publication No. US20030022184A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; Allen, Antonette C.
; Alvares, Christopher P.
; Ciltz, Brenda S.
; Olson, Sheri J.
; Thurder, Denise
; Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; BRCAL Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan Lewis & Bockius LLP
; STREET: 1111 Pennsylvania Avenue N. W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/982,828

FILING DATE: 22-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/074,453

FILING DATE: 1998-05-06

APPLICATION NUMBER: US 08/798,691

FILING DATE: 1997-02-12

APPLICATION NUMBER: US 08/598,591

FILING DATE: 1996-02-12

ATTORNEY/AGENT INFORMATION:

NAME: Michael S. Tuscan

REGISTRATION NUMBER: 43,210

REFERENCE/DOCKET NUMBER: 44921-5053-01-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: 18R primer
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-982-828-60

Query Match 1.7%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 494 GCTGGGAAATGG 506
Db 17 GCTGGGAAATGG 5

SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-022-819-55
Query Match 1.7%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 494 GCTGGGAAATGG 506
Db 17 GCTGGGAAATGG 5

Search completed: March 14, 2003, 10:59:22
Job time : 49.143 secs

RESULT 15
US-10-022-819-55/c
Sequence 55, Application US/10022819
Publication No. US20030027166A1
GENERAL INFORMATION:
APPLICANT: ALLEN, Antonette C. P.
OLSEN, Sheri J.
LAWRENCE, Tammy
ANGELLY, Tracy S.
RABIN, Mark B.
TITLE OF INVENTION: CODING SEQUENCE HAPLOTYPE OF THE HUMAN
BRCA1 GENE
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Avenue
CITY: Washington DC
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/022,819
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,452
FILING DATE: 1998-05-06
ATTORNEY/AGENT INFORMATION:
NAME: <Unknown>
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 044921-5049-01-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PRIMER"
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 03:41:43 ; Search time 114.171 Seconds
(without alignments)
15385.391 Million cell updates/sec

Title: US-09-869-894-1

Perfect score: 780

Sequence: 1 gagcgagcattcgcagcaca.....aattgatgtattttctct 780

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 segs, 112599159 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database:

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21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	3.6	28	24	ABK67134 Human gene specific
2	26	3.3	26	24	ABK67133 Human gene specific
3	22	2.8	22	21	AAZ39089 Human Al anti-apop
4	20	2.6	20	16	AA741123 Human gene signatu
5	20	2.6	20	16	AA741124 Human gene signatu
6	20	2.6	20	21	AAZ39089 Human Al anti-apop
7	20	2.6	20	21	AAZ39070 Human Al anti-apop
8	20	2.6	20	21	AAZ39071 Human Al anti-apop
9	20	2.6	20	21	AAZ39072 Human Al anti-apop

C 10	20	2.6	20	21	AAZ39073	Human Al anti-apop
C 11	20	2.6	20	21	AAZ39074	Human Al anti-apop
C 12	20	2.6	20	21	AAZ39075	Human Al anti-apop
C 13	20	2.6	20	21	AAZ39076	Human Al anti-apop
C 14	20	2.6	20	21	AAZ39077	Human Al anti-apop
C 15	20	2.6	20	21	AAZ39078	Human Al anti-apop
C 16	20	2.6	20	21	AAZ39079	Human Al anti-apop
C 17	20	2.6	20	21	AAZ39080	Human Al anti-apop
C 18	20	2.6	20	21	AAZ39081	Human Al anti-apop
C 19	20	2.6	20	21	AAZ39082	Human Al anti-apop
C 20	20	2.6	20	21	AAZ39083	Human Al anti-apop
C 21	16	2.1	16	17	AA716171	Primer #1 for huma
C 22	15	1.9	15	20	AAA96409	Primer used to amp
C 23	15	1.9	15	24	AB140366	Primer 2 relative
C 24	15	1.9	15	32	AA164146	Human PTB1B protei
C 25	15	1.9	15	38	AAZ09965	PTB1B forward PCR
C 26	15	1.9	15	42	AA76697	Human PTB1B coding
C 27	15	1.9	15	46	AA725577	Human gene signatu
C 28	14	1.8	14	19	AAA86392	PCBA HH ribozyme b
C 29	14	1.8	14	19	AAA86393	PCBA HH ribozyme b
C 30	14	1.8	14	19	AAA86394	PCBA HH ribozyme b
C 31	14	1.8	14	19	AAA86395	PCBA HH ribozyme b
C 32	14	1.8	14	19	AAA86396	PCBA HH ribozyme b
C 33	14	1.8	14	19	AAH61554	PCNA HH ribozyme b
C 34	14	1.8	14	19	AAH61555	PCNA HH ribozyme b
C 35	14	1.8	14	19	AAH61556	PCNA HH ribozyme b
C 36	14	1.8	14	19	AAH61557	PCNA HH ribozyme b
C 37	14	1.8	14	19	AAH61558	PCNA HH ribozyme b
C 38	14	1.8	14	20	AAZ17886	RT-PCR primer spec
C 39	14	1.8	14	20	AAZ17990	Homeobox conserved
C 40	14	1.8	14	20	AAZ44575	Newcastle disease
C 41	14	1.8	14	20	AAH21118	C. glutamicum brnf
C 42	14	1.8	14	20	AAH61241	C. glutamicum tran
C 43	14	1.8	14	20	AAH61241	Human bcl-2 mRNA n
C 44	14	1.8	14	20	AAH61241	Human bcl-2 mRNA n
C 45	14	1.8	14	20	AAH61241	Human bcl-2 mRNA n

ALIGNMENTS

RESULT 1
ABK67134/c
ABK67134 standard; DNA; 28 BP.

ABK67134;
02-JUL-2002 (first entry)
Human gene specific PCR primer #1222.

Primer; ss; DNA microarray; differential expression analysis; human.

Homo sapiens.

US6352829-B1.

05-MAR-2002.

05-JAN-1999; 99US-0225928.

21-MAY-1997; 97US-0859998.

(CLON-) CLONTECH LAB INC.

Chenich A, Johndaze G, Bibliahvilli R;

WPI; 2002-314699/35.

Producing sub-population of labeled nucleic acids; useful for analysing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers

PS Example 3: SEQ ID No 1222; 11pp; English.

XX The invention relates to producing a sub-population of labeled nucleic
CC acids (NAs) comprising contacting a NA sample from a physiological
CC source, with a pool of 50 distinct gene specific primers under suitable
CC conditions to enzymatically generate sub-population of NAs, where
CC each gene specific primer has a sequence complementary to a distinct
CC mRNA, and each labeled NA is generated using a single gene specific
CC primer. The method is useful for producing a sub-population of labeled
CC NAs which is useful for analysing the differences in the RNA profiles
CC between several different physiological sources, where the method
CC comprises producing subpopulation of labeled NAs for the different
CC physiological sources, comprising the populations for each physiological
CC source to identify differences in the population, where the comparison
CC is preferably performed by hybridising the labeled NAs for each of the
CC distinct physiological sources to an array of probe NAs stably
CC associated with the surface of a substrate to produce a hybridisation
CC pattern for each of the sources, and comparing the patterns for each of
CC the sources, where differential gene expression assays are
CC utilised in differential expression analysis of diseased a normal
CC tissue e.g. neoplastic a normal tissue, or different tissue or
CC sub tissue types. The present sequence is a human gene specific PCR
CC primer used in the method of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from USPTO at
CC http://ipo.segdata.uspto.gov/sequence.html?DocID=635282981.

XX Sequence 28 BP; 6 A; 4 C; 9 G; 9 T; 0 other;

Query Match 3.6%; Score 28; DB 24; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00074;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 TCCGTAGACACTGCCAGAACACTATTCA 292
DB 28 TCCGTAGACACTGCCAGAACACTATTCA 1

RESULT 2

ID ABR67133 standard; DNA; 26 BP.

XX ABR67133;

DT 02-JUL-2002 (first entry)

DE Human gene specific PCR primer #1221.

XX Primer; ss; DNA microarray; differential expression analysis; human.

OS Homo sapiens.

XX US6352829-B1.

PD 05-MAR-2002.

PF 05-JAN-1999; 99US-0225928.

PR 21-MAY-1997; 97US-0859998.

PA (CLON-) CLONTECH LAB INC.

PI Chenchik A, Johndade G, Biblilashvili R;

DR WPI; 2002-314699/35.

XX Producing sub-population of labeled nucleic acids, useful for analysing
PT differences in RNA profiles between several different physiological
PT sources, using set of distinct gene specific primers -
PS Example 3; SEQ ID No 1221; 11pp; English.

CC The invention relates to producing a sub-population of labeled nucleic
CC acids (NAs) comprising contacting a NA sample from a physiological
CC source, with a pool of 50 distinct gene specific primers under suitable
CC conditions to enzymatically generate sub-population of NAs, where
CC each gene specific primer has a sequence complementary to a distinct
CC mRNA, and each labeled NA is generated using a single gene specific
CC primer. The method is useful for producing a sub-population of labeled
CC NAs which is useful for analysing the differences in the RNA profiles
CC between several different physiological sources, where the method
CC comprises producing subpopulation of labeled NAs for the different
CC physiological sources, comprising the populations for each physiological
CC source to identify differences in the population, where the comparison
CC is preferably performed by hybridising the labeled NAs for each of the
CC distinct physiological sources to an array of probe NAs stably
CC associated with the surface of a substrate to produce a hybridisation
CC pattern for each of the sources, and comparing the patterns for each of
CC the sources, where differential gene expression assays are
CC utilised in differential expression analysis of diseased a normal
CC tissue e.g. neoplastic a normal tissue, or different tissue or
CC sub tissue types. The present sequence is a human gene specific PCR
CC primer used in the method of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from USPTO at
CC http://ipo.segdata.uspto.gov/sequence.html?DocID=635282981.

XX Sequence 26 BP; 9 A; 7 C; 7 G; 3 T; 0 other;

Query Match 3.3%; Score 26; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0076;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 TCCACCAGCAGAGATGACGACTG 89
DB 1 TCCACCAGCAGAGATGACGACTG 26

RESULT 3

ID AA239089/c

XX AA239089;

DT 29-FEB-2000 (first entry)

DE Human A1 anti-apoptotic bcl-2-related protein PCR probe.

XX Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;

KW mcl-1; apoptosis; cancer; antiinflammatory; cytosolic; tumour;

XX inflammation; diagnosis; phosphorothiolate; PCR; probe; ss.

OS Synthetic.

XX Homo sapiens.

PN US6001992-A.

PD 14-DEC-1999.

PF 07-JAN-1999; 99US-0226568.

PR 07-JAN-1999; 99US-0226568.

PA (ISIS-) ISIS PHARM INC.

PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;

DR WPI; 2000-061908/05.

XX Antisense oligonucleotides which modulate the expression of novel
PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT and treating associated diseases e.g. cancer -
PS Example 9; Column 28; 28pp; English.

XX The present invention describes antisense oligonucleotides which modulate
 CC the expression of novel anti-apoptotic bcl-2-related proteins. The
 CC antisense oligonucleotides can be used as therapeutic agents to prevent
 CC or delay inflammation or tumour formation by promoting apoptosis in
 CC human cells or tissues. They can also be used as research agents to
 CC establish the function of particular genes and as diagnostic agents in
 CC sandwich assays for detecting the level of novel anti-apoptotic
 CC bcl-2-related proteins in a sample. The antisense oligonucleotides
 CC given in the present invention were designed to target human A1 and
 CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
 CC present sequence represents a PCR probe for the human A1 nucleotide
 CC sequence.

SO Sequence 22 BP; 6 A; 2 C; 7 G; 7 T; 0 other;

Query Match 2.8%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.79;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 663 ACGATTGCCACATCTCTCT 684
 DB 22 ACGATTGCCACATCTCTCT 1

RESULT 4

AAT41123
 ID AAT41123 standard; DNA; 20 BP.

XX AAT41123;

DT 03-DEC-1996 (first entry)

DE Human gene signature HUMGS01288-derived sense primer.

KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; primer; PCR; amplification;
 KW polymerase chain reaction; ss.

XX Synthetic.

PN WO9514772-A1.

XX 01-JUN-1995.

PF 11-NOV-1994; 94WO-JP01916.

XX 12-NOV-1993; 93JP-0355504.

PA (MATS/) MATSUBARA K.

PA (OKUBO/) OKUBO K.

PI Matsubara K, Okubo K;

DR WPI: 1995-206931/27.

XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues

PS Example 7; Fig 7; 2245pp; Japanese.

XX Primers T41001-T41382 are derived from novel human gene signature (GS)
 CC sequences which did not match with sequences deposited in Genbank release
 CC 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
 CC libraries prepared from various human tissues; synthesis of cDNA was
 CC initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
 CC Each library is constructed so as to reflect accurately the relative
 CC abundance of different mRNAs in the particular tissue from which it was
 CC derived. The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS sequences)

CC as a means of diagnosing abnormal cell function or for recognising
 CC different cell types. The primers T41123-4 amplify clone pm2245 which
 CC comprises the GS HUMGS01288 (T20288), located on chromosome 10.
 CC

SO Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 other;

Query Match 2.6%; Score 20; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 571 TGTGAATGCTATCTCTCT 590
 DB 1 TGTGAATGCTATCTCTCT 20

RESULT 5

AAT41124/C
 ID AAT41124 standard; DNA; 20 BP.

XX AAT41124;

DT 03-DEC-1996 (first entry)

DE Human gene signature HUMGS01288-derived anti-sense primer.

KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; primer; PCR; amplification;
 KW polymerase chain reaction; ss.

XX Synthetic.

PN WO9514772-A1.

XX 01-JUN-1995.

PF 11-NOV-1994; 94WO-JP01916.

XX 12-NOV-1993; 93JP-0355504.

PA (MATS/) MATSUBARA K.

PA (OKUBO/) OKUBO K.

PI Matsubara K, Okubo K;

DR WPI: 1995-206931/27.

XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues

PS Example 7; Fig 7; 2245pp; Japanese.

XX Primers T41001-T41382 are derived from novel human gene signature (GS)
 CC sequences which did not match with sequences deposited in Genbank release
 CC 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
 CC libraries prepared from various human tissues; synthesis of cDNA was
 CC initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
 CC Each library is constructed so as to reflect accurately the relative
 CC abundance of different mRNAs in the particular tissue from which it was
 CC derived. The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS sequences)
 CC as a means of diagnosing abnormal cell function or for recognising
 CC different cell types. The primers T41123-4 amplify clone pm2245 which
 CC comprises the GS HUMGS01288 (T20288), located on chromosome 10.

SO Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 other;

Query Match 2.6%; Score 20; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 651 ACTGATATGGAACGATTGC 670
 DB 20 ACTGATATGGAACGATTGC 1

RESULT 6

AAZ39069/c
 ID AAZ39069 standard; DNA; 20 BP.

XX AAZ39069;

DT 29-FEB-2000 (first entry)

DE Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17484.

KW Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;

KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;

KW inflammation; diagnosis; phosphorothioate; ss.

XX Synthetic.

OS Homo sapiens.

PN US6001992-A.

PD 14-DEC-1999.

PE 07-JAN-1999; 99US-0226568.

PR 07-JAN-1999; 99US-0226568.

PS (ISIS-) ISIS PHARM INC.

PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;

DR WPI; 2000-061908/05.

XX Antisense oligonucleotides which modulate the expression of novel

PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis

and treating associated diseases e.g. cancer -

XX Claim 21; Column 27; 28pp; English.

XX The present invention describes antisense oligonucleotides which modulate

CC the expression of novel anti-apoptotic bcl-2-related proteins. The

CC antisense oligonucleotides can be used as therapeutic agents to prevent

CC or delay inflammation or tumour formation by promoting apoptosis in

CC human cells or tissues. They can also be used as research agents to

CC establish the function of particular genes and as diagnostic agents in

CC sandwich assays for detecting the level of novel anti-apoptotic

CC bcl-2-related proteins in a sample. The antisense oligonucleotides

CC given in the present invention were designed to target human A1 and

CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The

CC present sequence represents an antisense oligonucleotide for the

XX human A1 nucleotide sequence.

XX Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 other;

XX Query Match 2.6%; Score 20; DB 21; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 8.1;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 CATGCGCTCAGACGCTTCAA 38
 DB 20 CATGCGCTCAGACGCTTCAA 1

RESULT 7

AAZ39070/c
 ID AAZ39070 standard; DNA; 20 BP.

XX AAZ39070;

DT 29-FEB-2000 (first entry)

XX Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17485.

XX Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;

KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;

KW inflammation; diagnosis; phosphorothioate; ss.

XX Synthetic.

OS Homo sapiens.

PN US6001992-A.

PD 14-DEC-1999.

PE 07-JAN-1999; 99US-0226568.

PR 07-JAN-1999; 99US-0226568.

PS (ISIS-) ISIS PHARM INC.

PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;

DR WPI; 2000-061908/05.

XX Antisense oligonucleotides which modulate the expression of novel

PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis

and treating associated diseases e.g. cancer -

XX Claim 21; Column 27; 28pp; English.

XX The present invention describes antisense oligonucleotides which modulate

CC the expression of novel anti-apoptotic bcl-2-related proteins. The

CC antisense oligonucleotides can be used as therapeutic agents to prevent

CC or delay inflammation or tumour formation by promoting apoptosis in

CC human cells or tissues. They can also be used as research agents to

CC establish the function of particular genes and as diagnostic agents in

CC sandwich assays for detecting the level of novel anti-apoptotic

CC bcl-2-related proteins in a sample. The antisense oligonucleotides

CC given in the present invention were designed to target human A1 and

CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The

CC present sequence represents an antisense oligonucleotide for the

XX human A1 nucleotide sequence.

XX Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

XX Query Match 2.6%; Score 20; DB 21; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 8.1;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 GGTGAGCCAGCTCAGACTT 58
 DB 20 GGTGAGCCAGCTCAGACTT 1

RESULT 8

AAZ39071/c
 ID AAZ39071 standard; DNA; 20 BP.

XX AAZ39071;

DT 29-FEB-2000 (first entry)

DE Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17486.

KW Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;

KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;

KW inflammation; diagnosis; phosphorothioate; ss.

XX Synthetic.

OS Homo sapiens.

PN US6001992-A.

PD 14-DEC-1999.
XX
PF 07-JAN-1999; 990S-0226568.
XX
PR 07-JAN-1999; 990S-0226568.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR WPI: 2000-061908/05.
XX
XX Antisense oligonucleotides which modulate the expression of novel
PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
XX and treating associated diseases e.g. cancer -
PS
XX Claim 21; Column 27; 28pp; English.
XX
CC The present invention describes antisense oligonucleotides which modulate
CC the expression of novel anti-apoptotic bcl-2-related proteins. The
CC antisense oligonucleotides can be used as therapeutic agents to prevent
CC or delay inflammation or tumour formation by promoting apoptosis in
CC human cells or tissues. They can also be used as research agents to
CC establish the function of particular genes and as diagnostic agents in
CC sandwich assays for detecting the level of novel anti-apoptotic
CC bcl-2-related proteins in a sample. The antisense oligonucleotides
CC given in the present invention were designed to target human A1 and
CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC present sequence represents an antisense oligonucleotide for the
CC human A1 nucleotide sequence.
XX
SQ Sequence 20 BP; 1 A; 6 C; 5 G; 8 T; 0 other;
XX
Query Match 2.6%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 66 CACCAGGAGAGATGACAG 85
DB 20 CACCAGGAGAGATGACAG 1
XX
RESULT 9
AAZ39072/c
ID AAZ39072 standard; DNA; 20 BP.
XX
AC AAZ39072;
XX
DT 29-FEB-2000 (first entry)
XX
DE Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17487.
XX
XX Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW inflammation; diagnosis; phosphorothioate; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US6001992-A.
PN
XX 14-DEC-1999.
PD
XX 07-JAN-1999; 990S-0226568.
PF
XX 07-JAN-1999; 990S-0226568.
PR
XX 07-JAN-1999; 990S-0226568.
PS
XX (ISIS-) ISIS PHARM INC.
PA
XX Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
PI
XX WPI: 2000-061908/05.
DR
XX

PT Antisense oligonucleotides which modulate the expression of novel
PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
XX and treating associated diseases e.g. cancer -
XX
XX Claim 21; Column 27; 28pp; English.
XX
CC The present invention describes antisense oligonucleotides which modulate
CC the expression of novel anti-apoptotic bcl-2-related proteins. The
CC antisense oligonucleotides can be used as therapeutic agents to prevent
CC or delay inflammation or tumour formation by promoting apoptosis in
CC human cells or tissues. They can also be used as research agents to
CC establish the function of particular genes and as diagnostic agents in
CC sandwich assays for detecting the level of novel anti-apoptotic
CC bcl-2-related proteins in a sample. The antisense oligonucleotides
CC given in the present invention were designed to target human A1 and
CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC present sequence represents an antisense oligonucleotide for the
CC human A1 nucleotide sequence.
XX
SQ Sequence 20 BP; 8 A; 4 C; 1 G; 7 T; 0 other;
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Query Match 2.6%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 GAATTGGATATATTACAG 110
DB 20 GAATTGGATATATTACAG 1
XX
RESULT 10
AAZ39073/c
ID AAZ39073 standard; DNA; 20 BP.
XX
AC AAZ39073;
XX
DT 29-FEB-2000 (first entry)
XX
DE Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17488.
XX
XX Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW inflammation; diagnosis; phosphorothioate; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US6001992-A.
PN
XX 14-DEC-1999.
PD
XX 07-JAN-1999; 990S-0226568.
PF
XX 07-JAN-1999; 990S-0226568.
PR
XX 07-JAN-1999; 990S-0226568.
PS
XX (ISIS-) ISIS PHARM INC.
PA
XX Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
PI
XX WPI: 2000-061908/05.
DR
XX Antisense oligonucleotides which modulate the expression of novel
PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
XX and treating associated diseases e.g. cancer -
PS
XX Claim 21; Column 27; 28pp; English.
XX
CC The present invention describes antisense oligonucleotides which modulate
CC the expression of novel anti-apoptotic bcl-2-related proteins. The
CC antisense oligonucleotides can be used as therapeutic agents to prevent
CC or delay inflammation or tumour formation by promoting apoptosis in
CC human cells or tissues. They can also be used as research agents to
CC establish the function of particular genes and as diagnostic agents in

CC sandwich assays for detecting the level of novel anti-apoptotic
CC bcl-2-related proteins in a sample. The antisense oligonucleotides
CC given in the present invention were designed to target human A1 and
CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC present sequence represents an antisense oligonucleotide for the
CC human A1 nucleotide sequence.

SQ Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 other;

Query Match 2.6%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 GCTGGCTCAGACTACTGTC 130
DB 20 GCTGGCTCAGACTACTGTC 1

RESULT 11

AA239074/c
ID AA239074 standard; DNA; 20 BP.

XX AA239074;

DT 29-FEB-2000 (first entry)

XX Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17489.

XX Human; A1: anti-apoptotic; bcl-2-related protein; antisense inhibition;

XX mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;

XX inflammation; diagnosis; phosphorothioate; ss.

OS Synthetic.

OS Homo sapiens.

PN US6001992-A.

XX 14-DEC-1999.

PD 07-JAN-1999; 99US-0226568.

PE 07-JAN-1999; 99US-0226568.

XX 07-JAN-1999; 99US-0226568.

PS (ISIS-) ISIS PHARM INC.

XX Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;

PI WPI; 2000-061908/05.

DR WPI; 2000-061908/05.

XX Antisense oligonucleotides which modulate the expression of novel

PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis

CC and treating associated diseases e.g. cancer -

CC Claim 21: Column 27; 28pp; English.

XX The present invention describes antisense oligonucleotides which modulate

CC the expression of novel anti-apoptotic bcl-2-related proteins. The

CC antisense oligonucleotides can be used as therapeutic agents to prevent

CC or delay inflammation or tumour formation by promoting apoptosis in

CC human cells or tissues. They can also be used as research agents to

CC establish the function of particular genes and as diagnostic agents in

CC sandwich assays for detecting the level of novel anti-apoptotic

CC bcl-2-related proteins in a sample. The antisense oligonucleotides

CC given in the present invention were designed to target human A1 and

CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The

CC present sequence represents an antisense oligonucleotide for the

CC human A1 nucleotide sequence.

XX Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 other;

SQ Query Match 2.6%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 AATGTTGGTTCATGACGCA 212
DB 20 AATGTTGGTTCATGACGCA 1

RESULT 12

AA239075/c
ID AA239075 standard; DNA; 20 BP.

XX AA239075;

DT 29-FEB-2000 (first entry)

XX Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17490.

XX Human; A1: anti-apoptotic; bcl-2-related protein; antisense inhibition;

XX mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;

XX inflammation; diagnosis; phosphorothioate; ss.

OS Synthetic.

OS Homo sapiens.

PN US6001992-A.

XX 14-DEC-1999.

PD 07-JAN-1999; 99US-0226568.

PE 07-JAN-1999; 99US-0226568.

XX 07-JAN-1999; 99US-0226568.

PS (ISIS-) ISIS PHARM INC.

XX Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;

PI WPI; 2000-061908/05.

DR WPI; 2000-061908/05.

XX Antisense oligonucleotides which modulate the expression of novel

PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis

CC and treating associated diseases e.g. cancer -

CC Claim 21: Column 27; 28pp; English.

XX The present invention describes antisense oligonucleotides which modulate

CC the expression of novel anti-apoptotic bcl-2-related proteins. The

CC antisense oligonucleotides can be used as therapeutic agents to prevent

CC or delay inflammation or tumour formation by promoting apoptosis in

CC human cells or tissues. They can also be used as research agents to

CC establish the function of particular genes and as diagnostic agents in

CC sandwich assays for detecting the level of novel anti-apoptotic

CC bcl-2-related proteins in a sample. The antisense oligonucleotides

CC given in the present invention were designed to target human A1 and

CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The

CC present sequence represents an antisense oligonucleotide for the

CC human A1 nucleotide sequence.

XX Sequence 20 BP; 4 A; 3 C; 6 G; 7 T; 0 other;

SQ Query Match 2.6%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GACACTGCCAGAACTACTT 290

DB 20 GACACTGCCAGAACTACTT 1

RESULT 13

AA239076/c

ID AA239076 standard; DNA; 20 BP.

XX AA239076;

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DT 29-FEB-2000 (first entry)
XX
DE Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17491.
XX
KW Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KM mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
XX inflammation; diagnosis; phosphorothioate; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US6001992-A.
XX
PD 14-DEC-1999.
XX
PF 07-JAN-1999; 99US-0226568.
XX
PR 07-JAN-1999; 99US-0226568.
XX
PS Claim 21; Column 27; 28pp; English.
XX
PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR WPI; 2000-061908/05.
XX
PT Antisense oligonucleotides which modulate the expression of novel
PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT and treating associated diseases e.g. cancer -
XX
PS Claim 21; Column 27; 28pp; English.
XX
CC The present invention describes antisense oligonucleotides which modulate
CC the expression of novel anti-apoptotic bcl-2-related proteins. The
CC antisense oligonucleotides can be used as therapeutic agents to prevent
CC or delay inflammation or tumour formation by promoting apoptosis in
CC human cells or tissues. They can also be used as research agents to
CC establish the function of particular genes and as diagnostic agents in
CC sandwich assays for detecting the level of novel anti-apoptotic
CC bcl-2-related proteins in a sample. The antisense oligonucleotides
CC given in the present invention were designed to target human A1 and
CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC present sequence represents an antisense oligonucleotide for the
CC human A1 nucleotide sequence.
XX
SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 other;
XX
Query Match 2.6%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 309 GGAGTTTGAAAGCGCATCA 328
DB 20 GGAGTTTGAAAGCGCATCA 1

```

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XX
PD 14-DEC-1999.
XX
PF 07-JAN-1999; 99US-0226568.
XX
PR 07-JAN-1999; 99US-0226568.
XX
PS (ISIS-) ISIS PHARM INC.
XX
PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR WPI; 2000-061908/05.
XX
PT Antisense oligonucleotides which modulate the expression of novel
PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT and treating associated diseases e.g. cancer -
XX
PS Claim 21; Column 27; 28pp; English.
XX
CC The present invention describes antisense oligonucleotides which modulate
CC the expression of novel anti-apoptotic bcl-2-related proteins. The
CC antisense oligonucleotides can be used as therapeutic agents to prevent
CC or delay inflammation or tumour formation by promoting apoptosis in
CC human cells or tissues. They can also be used as research agents to
CC establish the function of particular genes and as diagnostic agents in
CC sandwich assays for detecting the level of novel anti-apoptotic
CC bcl-2-related proteins in a sample. The antisense oligonucleotides
CC given in the present invention were designed to target human A1 and
CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC present sequence represents an antisense oligonucleotide for the
CC human A1 nucleotide sequence.
XX
SQ Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 other;
XX
Query Match 2.6%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 379 AAGAACTTCTACGACAGCA 398
DB 20 AAGAACTTCTACGACAGCA 1

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RESULT 15
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ID AA239078 standard; DNA: 20 BP.
XX
AC AA239078;
XX
DT 29-FEB-2000 (first entry)
XX
DE Human A1 anti-apoptotic bcl-2-related protein antisense oligo #17493.
XX
KW Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KM mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
XX inflammation; diagnosis; phosphorothioate; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US6001992-A.
XX
PD 14-DEC-1999.
XX
PF 07-JAN-1999; 99US-0226568.
XX
PR 07-JAN-1999; 99US-0226568.
XX
PS (ISIS-) ISIS PHARM INC.
XX
PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR WPI; 2000-061908/05.

```

```
XX Antisense oligonucleotides which modulate the expression of novel
PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT and treating associated diseases e.g. cancer -
XX
XX Claim 21: Column 27; 28pp; English.
XX
CC The present invention describes antisense oligonucleotides which modulate
CC the expression of novel anti-apoptotic bcl-2-related proteins. The
CC antisense oligonucleotides can be used as therapeutic agents to prevent
CC or delay inflammation or tumour formation by promoting apoptosis in
CC human cells or tissues. They can also be used as research agents to
CC establish the function of particular genes and as diagnostic agents in
CC sandwich assays for detecting the level of novel anti-apoptotic
CC bcl-2-related proteins in a sample. The antisense oligonucleotides
CC given in the present invention were designed to target human A1 and
CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC present sequence represents an antisense oligonucleotide for the
CC human A1 nucleotide sequence.
XX
SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 other;
Query Match 2.6%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 556 GTTACAGGAAAGATCTGTGA 575
|||||
Db 20 GTTACAGGAAAGATCTGTGA 1
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OK nucleic - nucleic search, using sw model

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13	20	2.6	20	1 PCT-US99-29593-5	Sequence 5, Ap1
14	20	2.6	20	1 PCT-US99-29593-6	Sequence 6, Ap1
15	20	2.6	20	1 PCT-US99-29593-7	Sequence 7, Ap1
16	20	2.6	20	1 PCT-US99-29593-8	Sequence 8, Ap1
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28	20	2.6	20	1 PCT-US99-29593-20	Sequence 20, Ap1
29	20	2.6	20	1 PCT-US99-29593-21	Sequence 21, Ap1
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52	20	2.6	20	1 PCT-US99-29593-44	Sequence 44, Ap1
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54	20	2.6	20	1 PCT-US99-29593-46	Sequence 46, Ap1
55	20	2.6	20	1 PCT-US99-29593-47	Sequence 47, Ap1
56	20	2.6	20	1 PCT-US99-29593-48	Sequence 48, Ap1
57	20	2.6	20	1 PCT-US99-29593-49	Sequence 49, Ap1
58	20	2.6	20	1 PCT-US99-29593-50	Sequence 50, Ap1
59	20	2.6	20	1 PCT-US99-29593-51	Sequence 51, Ap1
60	20	2.6	20	1 PCT-US99-29593-52	Sequence 52, Ap1
61	20	2.6	20	1 PCT-US99-29593-53	Sequence 53, Ap1
62	20	2.6	20	1 PCT-US99-29593-54	Sequence 54, Ap1
63	20	2.6	20	1 PCT-US99-29593-55	Sequence 55, Ap1
64	20	2.6	20	1 PCT-US99-29593-56	Sequence 56, Ap1
65	20	2.6	20	1 PCT-US99-29593-57	Sequence 57, Ap1
66	20	2.6	20	1 PCT-US99-29593-58	Sequence 58, Ap1
67	20	2.6	20	1 PCT-US99-29593-59	Sequence 59, Ap1
68	20	2.6	20	1 PCT-US99-29593-60	Sequence 60, Ap1
69	20	2.6	20	1 PCT-US99-29593-61	Sequence 61, Ap1
70	20	2.6	20	1 PCT-US99-29593-62	Sequence 62, Ap1
71	20	2.6	20	1 PCT-US99-29593-63	Sequence 63, Ap1
72	20	2.6	20	1 PCT-US99-29593-64	Sequence 64, Ap1
73	20	2.6	20	1 PCT-US99-29593-65	Sequence 65, Ap1
74	20	2.6	20	1 PCT-US99-29593-66	Sequence 66, Ap1
75	20	2.6	20	1 PCT-US99-29593-67	Sequence 67, Ap1
76	20	2.6	20	1 PCT-US99-29593-68	Sequence 68, Ap1
77	20	2.6	20	1 PCT-US99-29593-69	Sequence 69, Ap1
78	20	2.6	20	1 PCT-US99-29593-70	Sequence 70, Ap1
79	20	2.6	20	1 PCT-US99-29593-71	Sequence 71, Ap1
80	20	2.6	20	1 PCT-US99-29593-72	Sequence 72, Ap1
81	20	2.6	20	1 PCT-US99-29593-73	Sequence 73, Ap1
82	20	2.6	20	1 PCT-US99-29593-74	Sequence 74, Ap1
83	20	2.6	20	1 PCT-US99-29593-75	Sequence 75, Ap1
84	20	2.6	20	1 PCT-US99-29593-76	Sequence 76, Ap1
85	20	2.6	20	1 PCT-US99-29593-77	Sequence 77, Ap1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C	22	20	2.6	20	1	PCT-US99-285593-13	Sequence 13, Appl
C	22	20	2.6	20	1	PCT-US99-285593-14	Sequence 14, Appl
C	24	20	2.6	20	1	PCT-US99-285593-15	Sequence 15, Appl
C	25	20	2.6	20	1	PCT-US99-285593-16	Sequence 16, Appl
C	26	20	2.6	20	33	US-09-869-894-2	Sequence 2, Appl
C	27	20	2.6	20	33	US-09-869-894-3	Sequence 3, Appl
C	28	20	2.6	20	33	US-09-869-894-4	Sequence 4, Appl
C	29	20	2.6	20	33	US-09-869-894-5	Sequence 5, Appl
C	30	20	2.6	20	33	US-09-869-894-6	Sequence 6, Appl
C	31	20	2.6	20	33	US-09-869-894-7	Sequence 7, Appl
C	32	20	2.6	20	33	US-09-869-894-8	Sequence 8, Appl
C	33	20	2.6	20	33	US-09-869-894-9	Sequence 9, Appl
C	34	20	2.6	20	33	US-09-869-894-10	Sequence 10, Appl
C	35	20	2.6	20	33	US-09-869-894-11	Sequence 11, Appl
C	36	20	2.6	20	33	US-09-869-894-12	Sequence 12, Appl
C	37	20	2.6	20	33	US-09-869-894-13	Sequence 13, Appl
C	38	20	2.6	20	33	US-09-869-894-14	Sequence 14, Appl
C	39	20	2.6	20	33	US-09-869-894-15	Sequence 15, Appl
C	40	20	2.6	20	33	US-09-869-894-16	Sequence 16, Appl
C	41	17	2.2	45	18	US-09-404-520-41805	Sequence 1805, A
C	42	16	2.2	22	6	US-08-278-774-28	Sequence 28, Appl
C	43	16	2.1	25	17	US-09-396-196F-36231	Sequence 36231, A
C	44	16	2.1	25	17	US-09-396-196G-36231	Sequence 36231, A
C	45	16	2.1	25	36	US-09-954-427-70874	Sequence 70874, A

ALIGNMENTS

```

RESULT 1
PCT-US01-47856-2596
Sequence 2596, Application PC/TJUS0147856
GENERAL INFORMATION:
APPLICANT: BIOCARDIA, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Quettermous, Thomas
APPLICANT: Johnson, Frances
APPLICANT: Fry, Kirk
APPLICANT: Matcuk, George
APPLICANT: Prentice, James
APPLICANT: Phillips, Tulle
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Altman, Peter
TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
FILE REFERENCE: 506612000140
CURRENT APPLICATION NUMBER: PCT/US01/47856
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 60/211,994
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 8832
SOFTWARE: Patencn version 3.1
SEQ ID NO 2596
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-47856-2596

```

```

Query Match Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 7 7e-16;
Matches 50; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 703 TTATATATGTAACTTGACCTTCACAGGTTATGGAATTTGTCCCATGT 752
Db 1 TTATATATGTAACTTGACCTTCACAGGTTATGGAATTTGTCCCATGT 50

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RESULT 2
PCT-US01-47856-3838
; Sequence 3838, Application PC/TUS0147856
; GENERAL INFORMATION:

Sequence 13,	Appl
Sequence 14,	Appl
Sequence 15,	Appl
Sequence 16,	Appl
Sequence 2,	Appl
Sequence 3,	Appl
Sequence 4,	Appl
Sequence 5,	Appl
Sequence 7,	Appl
Sequence 8,	Appl
Sequence 9,	Appl
Sequence 10,	Appl
Sequence 11,	Appl
Sequence 12,	Appl
Sequence 13,	Appl
Sequence 14,	Appl
Sequence 15,	Appl
Sequence 16,	Appl
Sequence 28,	Appl
Sequence 29,	Appl
Sequence 36231,	A
Sequence 36231,	A
Sequence 70874,	A

```

APPLICANT: BIOCARDIA, INC.
APPLICANT: Mohlgenmuth, Jay
APPLICANT: Quettermous, Thomas
APPLICANT: Johnson, Frances
APPLICANT: Fry, Kirk
APPLICANT: Matcuk, George
APPLICANT: Prentice, James
APPLICANT: Phillips, Julie
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Altman, Peter
TITLE OF INVENTION: LEDKOCYTE EXPRESSION PROFILING
FILE REFERENCE: 506612000140
CURRENT APPLICATION NUMBER: PCT/US01/47856
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/241,994
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/256,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 8832
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3838
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-47856-3838

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Query Match	6.48;	Score 50;	DB 1;6	Length 50;
Best Local Similarity	100.0%;	Pred. No. 7.7e-1;		
Matches 50;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	703	TTGATGATGACTGACCTCCAGAGTATGAGAAATTTGGCCCATGT	752
Db	1	TTGATGATGACTGACCTCCAGAGTATGAGAAATTTGGCCCATGT	50

```

? RESULT 3
? US-10-131-827-2596
? Sequence 2596, Application US/10131827
? GENERAL INFORMATION:
? APPLICANT: Wohlgemuth, Jay
? APPLICANT: Fry, Kirk
? APPLICANT: Woodward, Robert
? APPLICANT: Ly, Nac
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
? TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
? FILE REFERENCE: 506612000120
? CURRENT APPLICATION NUMBER: US/10/131.827
? CURRENT FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: US 10/006,290
? PRIOR FILING DATE: 2001-10-22
? PRIOR APPLICATION NUMBER: US 60/296,764
? PRIOR FILING DATE: 2001-06-08
? NUMBER OF SEQ. ID NOS: 9090
? SOFTWARE: PatentIn version 3.1.
? SEQ. ID NO 2596
? LENGTH: 50
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-131-827-2596

```

```

Query Match      6.4%; Score 50; DB 40; Length 50;
Best Local Similarity 100.0%; Pident. No. 7,76-16;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 703 TTAGTATGTATGACCTTCACAGATTAAGCAAAATTTTGCCCCCATGT 752
      TTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Db 1 TTAGTATGTATGACCTTCACAGATTAAGCAAAATTTTGCCCCCATGT 50

```

RESULT 4
US-10-131-827-3838
; Sequence 3838, Application US/10131827

```

? GENERAL INFORMATION:
? APPLICANT: Wohlgemuth, Jay
? APPLICANT: Fry, Kirk
? APPLICANT: Woodward, Robert
? APPLICANT: Ly, Nnoc
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
? TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
? FILE REFERENCE: 506612000120
? CURRENT APPLICATION NUMBER: US/10/131,827
? CURRENT FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: US 10/006,290
? PRIOR FILING DATE: 2001-10-22
? PRIOR APPLICATION NUMBER: US 60/296,764
? PRIOR FILING DATE: 2001-06-08
? NUMBER OF SEQ ID NOS: 9090
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 3838
? LENGTH: 50
? TYPE: DNA
? ORGANISM: Homo sapiens
? OS-10-131-827-3838

```

```

RESULT 5
US-10-131-831-2596
: Sequence 2596, Application US/10131831
: GENERAL INFORMATION:
: APPLICANT: Wohlgemuth, Jay
: APPLICANT: Fry, Kirk
: APPLICANT: Woodward, Robert
: APPLICANT: Ivy, Nooc
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
: TITLE OF INVENTION: TRANSPLANT REJECTION
: FILE REFERENCE: 50661200121
: CURRENT APPLICATION NUMBER: US/10/131,831
: CURRENT FILING DATE: 2002-08-05
: PRIOR APPLICATION NUMBER: US 10/006,290
: PRIOR FILING DATE: 2001-10-22
: PRIOR APPLICATION NUMBER: US 60/296,764
: PRIOR FILING DATE: 2001-06-08
: NUMBER OF SEQ ID NOS: 9190
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2596
: LENGTH: 50
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-131-831-2596

```

```

RESULT 6
US-10-131-831-838
; Sequence 3838, Application US/10131831
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc

```

```

? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
? TITLE OF INVENTION: TRANSPLANT REJECTION
? FILE REFERENCE: 506612000121
? CURRENT APPLICATION NUMBER: US/10/131,831
? CURRENT FILING DATE: 2002-08-05
? PRIOR APPLICATION NUMBER: US 10/006,290
? PRIOR FILING DATE: 2001-10-22
? PRIOR APPLICATION NUMBER: US 60/296,764
? PRIOR FILING DATE: 2001-06-08
? NUMBER OF SEQ ID NOS: 9190
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 3838
? LENGTH: 50
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-131-831-3838

```

```

1      RESULT 7
2      US-09-225-201B-1222/c
3      Sequence 1222, Application US/09225201B
4      GENERAL INFORMATION:
5      APPLICANT: Chenchik, Alex
6      Bibilashvilli, Robert
7      Title of Invention: METHOD OF ASSAYING DIFFERENTIAL
8      EXPRESSION
9      NUMBER OF SEQUENCES: 1375
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Fish & Richardson, P.C.
12     STREET: 2200 Sand Hill Road, Suite 100
13     CITY: Menlo Park
14     STATE: CA
15     COUNTRY: US
16     ZIP: 94025
17
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Diskette
20     COMPUTER: IBM Compatible
21     OPERATING SYSTEM: Windows95
22     SOFTWARE: FastSO for Windows Version 2.0
23
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/09/225,201B
26     FILING DATE: 05-Jan-1999
27     CLASSIFICATION: <unknown>
28
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: US/08/859,998
31     FILING DATE: 21-MAY-1997
32
33     ATTORNEY/AGENT INFORMATION:
34     NAME: Field, Bret E.
35     REGISTRATION NUMBER: 37,620
36     REFERENCE/DOCKET NUMBER: 09096/002001
37
38     TELECOMMUNICATION INFORMATION:
39     TELEPHONE: 415-322-5070
40     TELEFAX: 415-854-0875
41
42     INFORMATION FOR SEQ ID NO: 1222:
43     SEQUENCE CHARACTERISTICS:
44     LENGTH: 28 base pairs
45     TYPE: nucleic acid
46     STRANDEDNESS: single
47     TOPOLOGY: linear
48     MOLECULE TYPE: DNA
49     FEATURE:
50     OTHER INFORMATION: oligonucleotide primer
51
52     SEQUENCE DESCRIPTION: SEQ ID NO: 1222:
53     US-09-225-201B-1222

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Query Match 3.6%; Score 28; DB 16; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00089;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 265 TCCGTAGACACTGCCAGACACTATTCA 292
 ||||||||||||||||||||||||||||
 Db 28 TCCGTAGACACTGCCAGACACTATTCA 1

RESULT 8

US-09-225-201B-1221

Sequence 1221, Application US/09225201B
 GENERAL INFORMATION:

APPLICANT: Chenchik, Alex

Jokhadze, George
 Bibilashvili, Robert

TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
 EXPRESSION

NUMBER OF SEQUENCES: 1375

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park

STATE: CA

COUNTRY: US

ZIP: 94025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/225, 201B

FILING DATE: 05-Jan-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/859, 998

FILING DATE: 21-May-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Field, Bret E.

REGISTRATION NUMBER: 37, 620

REFERENCE/DOCKET NUMBER: 09096/002001

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-322-5070

TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 1221:

SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: linear

FEATURE:
 OTHER INFORMATION: oligonucleotide primer

SEQUENCE DESCRIPTION: SEQ ID NO: 1221:

US-09-225-201B-1221

Query Match 3.3%; Score 26; DB 16; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 TCCACAGGAGAGATGACAGACTG 89
 ||||||||||||||||||||||||||||
 Db 1 TCCACAGGAGAGATGACAGACTG 26

RESULT 9

PCT-US99-29593-17/c
 Sequence 17, Application PC/TUS9929593
 GENERAL INFORMATION:
 APPLICANT: Ackermann, Elizabeth J.
 APPLICANT: Bennett, C. Frank

APPLICANT: Dean, Nicholas M.
 APPLICANT: Marcusson, Eric G.
 APPLICANT: Isis Pharmaceuticals, Inc.
 TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
 TITLE OF INVENTION: Proteins

FILE REFERENCE: ISPH-0432

CURRENT APPLICATION NUMBER: PCT/US99/29593

EARLIER FILING DATE: 1999-12-14

EARLIER APPLICATION NUMBER: 09/226, 568

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 17

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: antisense sequence

PCT-US99-29593-17

Query Match 2.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 663 ACGATTGCCACACATCTCT 684
 ||||||||||||||||||||||||
 Db 22 ACGATTGCCACACATCTCT 1

RESULT 10

US-09-869-894-17/c
 Sequence 17, Application US/09869894
 GENERAL INFORMATION:

APPLICANT: Ackermann, Elizabeth J.

APPLICANT: Bennett, C. Frank

APPLICANT: Marcusson, Eric G.

APPLICANT: Isis Pharmaceuticals, Inc.

TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
 FILE REFERENCE: ISPH-0432

CURRENT APPLICATION NUMBER: US/09/869, 894

EARLIER FILING DATE: 2001-07-06

EARLIER APPLICATION NUMBER: 09/226, 568

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 17

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: antisense sequence

US-09-869-894-17

Query Match 2.8%; Score 22; DB 33; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 663 ACGATTGCCACACATCTCT 684
 ||||||||||||||||||||||||
 Db 22 ACGATTGCCACACATCTCT 1

RESULT 11

PCT-US99-29593-2/c
 Sequence 2, Application PC/TUS9929593
 GENERAL INFORMATION:
 APPLICANT: Ackermann, Elizabeth J.
 APPLICANT: Bennett, C. Frank

APPLICANT: Dean, Nicholas M.
 APPLICANT: Marcusson, Eric G.
 APPLICANT: Isis Pharmaceuticals, Inc.

```

; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-2

Query Match
Best Local Similarity 2.6%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTGAGCATTCTCAGCACA 20
Db 20 GAGTGAGCATTCTCAGCACA 1

RESULT 12
PCT-US99-29593-3/c
; Sequence 3, Application PC/TUS9929593
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-3

Query Match
Best Local Similarity 2.6%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CATTGCCTCAACAGCTTCAA 38
Db 20 CATTGCCTCAACAGCTTCAA 1

RESULT 13
PCT-US99-29593-4/c
; Sequence 4, Application PC/TUS9929593
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; FILE REFERENCE: ISPH-0432
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-4
```

```

; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-4

Query Match
Best Local Similarity 2.6%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 GGTGAGCCAGCTCAAGCTT 58
Db 20 GGTGAGCCAGCTCAAGCTT 1

RESULT 14
PCT-US99-29593-5/c
; Sequence 5, Application PC/TUS9929593
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-5

Query Match
Best Local Similarity 2.6%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 CACGAGCGAGAGATGACAG 85
Db 20 CACGAGCGAGAGATGACAG 1

RESULT 15
PCT-US99-29593-6/c
; Sequence 6, Application PC/TUS9929593
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of Novel Anti-apoptotic bcl-2-Related
; FILE REFERENCE: ISPH-0432
; CURRENT APPLICATION NUMBER: PCT/US99/29593
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 09/226,568
```

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; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense sequence
PCT-US99-29593-6

Query Match      2.6%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 91 GAATTTGCATATATTACAG 110
Db 20 GAATTTGCATATATTACAG 1

Search completed: March 14, 2003, 10:27:59
Job time : 1151.99 secs

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; CURRENT APPLICATION NUMBER: US/10/325,899
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 9966
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3838
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-325-899-3838

Query Match
Best Local Similarity 100.0%; Pred. No. 12e-16; Length 50;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 703 TTGATGATGTAAGTCCAGAGCTTATGGAATTTTGTCCCATGT 752
DB 1 TTGATGATGTAAGTCCAGAGCTTATGGAATTTTGTCCCATGT 50

RESULT 3
US-60-427-836-533438
; Sequence 533438, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 533438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-533438

Query Match
Best Local Similarity 100.0%; Pred. No. 0.23; Length 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 GTTGAACCTAATCTGCGTGG 540
DB 1 GTTGAACCTAATCTGCGTGG 22

RESULT 4
US-10-310-188-73875/C
; Sequence 73875, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73875
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-73875

Query Match
Best Local Similarity 100.0%; Pred. No. 0.8; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 733 TGAATTTTGTCCCATGTA 753
DB 21 TGAATTTTGTCCCATGTA 1

RESULT 5
US-10-310-188-85737/C
; Sequence 85737, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85737
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-85737

Query Match
Best Local Similarity 100.0%; Pred. No. 9.8; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 CTTGCTCTCCACGAGCA 74
DB 19 CTTGCTCTCCACGAGCA 1

RESULT 6
US-60-427-836-6872
; Sequence 6872, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 6872
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-6872

Query Match
Best Local Similarity 100.0%; Pred. No. 9.9; Length 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 AAAGTCCAGAGTCTACA 191
DB 1 AAAGTCCAGAGTCTACA 19

RESULT 7
US-60-427-836-59598
; Sequence 59598, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 59598
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
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US-60-427-836-59598

Query Match 2.3%; Score 18; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TCCAGCAAAAGCTCCAG 182

|||||

DB 8 TCCAGCAAAAGCTCCAG 25

RESULT 8
US-60-427-808-360861
; Sequence 360861, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 360861
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-360861

Query Match

2.2%; Score 17; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 AGAGCTATCTGCAGTCG 135

|||||

DB 3 AGAGCTATCTGCAGTCG 19

RESULT 9

US-60-427-808-757664/C
; Sequence 757664, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 757664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-757664

Query Match 2.2%; Score 17; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 CCAAAAAGAGTGGAAA 226

|||||

DB 20 CCAAAAAGAGTGGAAA 4

RESULT 10
US-10-303-778-10504/C
; Sequence 10504, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: Patentia version 3.1
; SEQ ID NO 10504
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Infectious hypodermal and hematopoietic necrosis virus
US-10-303-778-10504

Query Match 2.1%; Score 16; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GAAAAGAGTTTGAG 319

|||||

DB 19 GAAAAGAGTTTGAG 4

RESULT 11
US-10-355-577-67556/C
; Sequence 67556, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67556
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-67556

Query Match 2.1%; Score 16; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 TAGAGTTACGAGAA 566

|||||

DB 23 TAGAGTTACGAGAA 8

RESULT 12
US-10-355-577-149144
; Sequence 149144, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 149144
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-149144

Query Match 2.1%; Score 16; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 AGAACTTCTAGACA 395

|||||

DB 1 AGAACTTCTAGACA 16

RESULT 13
US-10-355-577-249093
; Sequence 249093, Application US/10355577
; GENERAL INFORMATION:

Search completed: March 14, 2003, 10:49:52
Job time : 215.449 secs

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; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 249093
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-249093

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```

Query Match      2.1%; Score 16; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 64 TCCACCAGCAGACAGA 79
DB 4 TCCACCAGCAGACAGA 19

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RESULT 14
US-10-355-577-317546
; Sequence 317546, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 317546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-317546

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```

Query Match      2.1%; Score 16; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 252 TGTATGTGTGTCC 267
DB 5 TGTATGTGTGTCC 20

```

```

RESULT 15
US-10-355-577-487471/c
; Sequence 487471, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 487471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-487471

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Query Match      2.1%; Score 16; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

OY 606 ACCAGAAAGACACTC 621
DB 21 ACCAGAAAGACACTC 6

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GenCore version 5.1.4_p5_4578
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OW nucleic - nucleic search, using sw model

Run On: March 14, 2003, 04:08:08 ; Search time 6850.7 Seconds

(without alignments)
16712.222 Million cell updates/sec

Title: US-09-869-894-18

Perfect score: 3934

Sequence: 1 tccagtaagagagtcggggtc.....aaatctttatcaataaa 3934

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched:

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

GenBml:*

1: gb_ba:*

2: gb_hlg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_ph:*

7: gb_pl:*

8: gb_pr:*

9: gb_ro:*

10: gb_sts:*

11: gb_sy:*

12: gb_un:*

13: gb_vl:*

14: em_ba:*

15: em_fun:*

16: em_hum:*

17: em_in:*

18: em_mu:*

19: em_om:*

20: em_ov:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_un:*

28: em_vl:*

29: em_vl:*

30: em_hlg_hum:*

31: em_hlg_inv:*

32: em_hlg_other:*

33: em_hlg_mus:*

34: em_hlg_pln:*

35: em_hlg_rod:*

36: em_hlg_mam:*

37: em_hlg_vit:*

38: em_sy:*

39: em_hlg_hum:*

40: em_hlg_mus:*

41: em_hlg_others:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	0.5	21	186713	186713 Sequence 1
C 2	20	0.5	20	AR095066	AR095066 Sequence
C 3	20	0.5	20	AR095067	AR095067 Sequence
C 4	20	0.5	20	AR095068	AR095068 Sequence
C 5	20	0.5	20	AR095069	AR095069 Sequence
C 6	20	0.5	20	AR095070	AR095070 Sequence
C 7	20	0.5	20	AR095071	AR095071 Sequence
C 8	20	0.5	20	AR095072	AR095072 Sequence
C 9	20	0.5	20	AR095073	AR095073 Sequence
C 10	20	0.5	20	AR095074	AR095074 Sequence
C 11	20	0.5	20	AR095075	AR095075 Sequence
C 12	20	0.5	20	AR095076	AR095076 Sequence
C 13	20	0.5	20	AR095077	AR095077 Sequence
C 14	20	0.5	20	AR095078	AR095078 Sequence
C 15	20	0.5	20	AR095079	AR095079 Sequence
C 16	20	0.5	20	AR095080	AR095080 Sequence
C 17	20	0.5	20	AR095081	AR095081 Sequence
C 18	20	0.5	20	AR095082	AR095082 Sequence
C 19	20	0.5	20	AR095083	AR095083 Sequence
C 20	20	0.5	20	AR095084	AR095084 Sequence
C 21	20	0.5	20	AR095085	AR095085 Sequence
C 22	20	0.5	20	186715	186715 Sequence 3
C 23	18	0.5	26	186729	186729 Sequence 17
C 24	18	0.5	33	115222	115222 Sequence 1
C 25	18	0.5	38	A67648	A67648 Sequence 68
C 26	18	0.5	38	AR089824	AR089824 Sequence
C 27	18	0.5	44	AX236881	AX236881 Sequence
C 28	18	0.5	44	AX239777	AX239777 Sequence
C 29	17	0.4	20	AX488424	AX488424 Sequence
C 30	17	0.4	21	A20477	A20477 Oligonucleo
C 31	17	0.4	24	AX250150	AX250150 Sequence
C 32	17	0.4	25	186728	186728 Sequence 16
C 33	17	0.4	45	AX009974	AX009974 Sequence
C 34	17	0.4	45	AX236883	AX236883 Sequence
C 35	17	0.4	45	AX236902	AX236902 Sequence
C 36	17	0.4	45	AX239779	AX239779 Sequence
C 37	17	0.4	45	AX239796	AX239796 Sequence
C 38	17	0.4	47	AX136052	AX136052 Sequence
C 39	17	0.4	50	I08559	I08559 Sequence 1
C 40	16	0.4	19	AR165304	AR165304 Sequence
C 41	16	0.4	20	AX488272	AX488272 Sequence
C 42	16	0.4	21	AR084547	AR084547 Sequence
C 43	16	0.4	21	AR084559	AR084559 Sequence
C 44	16	0.4	21	AR084561	AR084561 Sequence
C 45	16	0.4	21	AR084584	AR084584 Sequence

ALIGNMENTS

RESULT 1

186713/c

LOCUS 186713

DEFINITION Sequence 1 from patent US 5702897.

ACCESSION 186713

VERSION 186713.1

KEYWORDS GI:3206431

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 21)

AUTHORS Reed,J.C. and Sato,T.

TITLE Interaction of proteins involved in a cell death pathway

JOURNAL Patent: US 5702897-A 1 30-DEC-1997;

FEATURES Location/Qualifiers

source 1..21
/organism="unknown"
BASE COUNT 4 a 8 c 2 g 7 t
ORIGIN

Query Match 0.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1235 GCAGCTGCAGAGCATATG 1255
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Db 21 GCAGCTGCAGAGCATATG 1

RESULT 2
LOCUS AR095066 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 19 from patent US 6001992.
ACCESSION AR095066
VERSION AR095066.1 GI:10022583
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 19 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 5 a 8 c 4 g 3 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GCGGAGTGGCAATCTGGC 69
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Db 20 GCGGAGTGGCAATCTGGC 1

RESULT 3
LOCUS AR095067 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 20 from patent US 6001992.
ACCESSION AR095067
VERSION AR095067.1 GI:10022585
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 20 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 5 a 9 c 4 g 2 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 CCGGAGGCGCATTTGGCT 171
|||||
Db 20 CCGGAGGCGCATTTGGCT 1

RESULT 4

AR095068/c AR095068 20 bp DNA linear PAT 08-SEP-2000
LOCUS
DEFINITION Sequence 21 from patent US 6001992.
ACCESSION AR095068
VERSION AR095068.1 GI:10022587
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 21 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 2 a 10 c 3 g 5 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 AGGAGCTGGACGGTACGAG 450
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Db 20 AGGAGCTGGACGGTACGAG 1

RESULT 5
LOCUS AR095069 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 22 from patent US 6001992.
ACCESSION AR095069
VERSION AR095069.1 GI:10022589
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 22 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 6 c 3 g 7 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 501 CCGGGAATCTGGTATACCA 520
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Db 20 CCGGGAATCTGGTATACCA 1

RESULT 6
LOCUS AR095070 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 23 from patent US 6001992.
ACCESSION AR095070
VERSION AR095070.1 GI:10022591
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 23 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20

BASE COUNT	0	a	4	c	7	g	9	t	/organism="unknown"
ORIGIN									
Query Match	0.5%;	Score 20;	DB 6;	Length 20;					
Best Local Similarity	100.0%;	Pred. No. 39;							
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
OY	636	CGCCAGAGACACAAAGCCAA	655						
Db	20	CGCCAGAGACACAAAGCCAA	1						
RESULT 7									
AR095071/c									
LOCUS	AR095071	20 bp		DNA	linear		PAT 08-SEP-2000		
DEFINITION	Sequence 24 from patent US 6001992.								
ACCESSION	AR095071								
VERSION	AR095071.1	GI:10022593							
KEYWORDS	.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 20)								
TITLE	Ackermann, E.J., Bennett, C., Frank, J., Dean, N.M. and Marcusson, E.G.								
JOURNAL	Antisense modulation of novel anti-apoptotic bcl-2-related proteins								
FEATURES	Patent: US 6001992-A 24 14-DEC-1999;								
source	Location/Qualifiers								
	1..20								
BASE COUNT	7	a	7	c	3	g	3	t	/organism="unknown"
ORIGIN									
Query Match	0.5%;	Score 20;	DB 6;	Length 20;					
Best Local Similarity	100.0%;	Pred. No. 39;							
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
OY	842	GGGCGAGAGTGTGACTCTC	861						
Db	20	GGGCGAGAGTGTGACTCTC	1						
RESULT 8									
AR095072/c									
LOCUS	AR095072	20 bp		DNA	linear		PAT 08-SEP-2000		
DEFINITION	Sequence 25 from patent US 6001992.								
ACCESSION	AR095072								
VERSION	AR095072.1	GI:10022595							
KEYWORDS	.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 20)								
TITLE	Ackermann, E.J., Bennett, C., Frank, J., Dean, N.M. and Marcusson, E.G.								
JOURNAL	Antisense modulation of novel anti-apoptotic bcl-2-related proteins								
FEATURES	Patent: US 6001992-A 25 14-DEC-1999;								
source	Location/Qualifiers								
	1..20								
BASE COUNT	7	a	7	c	3	g	3	t	/organism="unknown"
ORIGIN									
Query Match	0.5%;	Score 20;	DB 6;	Length 20;					
Best Local Similarity	100.0%;	Pred. No. 39;							
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
OY	1045	AGGAATGTGCTGTGCTTT	1064						
Db	20	AGGAATGTGCTGTGCTTT	1						
RESULT 9									
AR095073/c									

LOCUS	AR095073	20 bp	DNA	linear	PAT 08-SEP-2000
DEFINITION	Sequence 26 from patent US 6001992.				
ACCESSION	AR095073				
VERSION	AR095073.1	GI:10022597			
KEYWORDS					
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 20)				
TITLE	Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.				
JOURNAL	Antisense modulation of novel anti-apoptotic bcl-2-related proteins				
FEATURES	Patent: US 6001992-A 26 14-DEC-1999;				
	Location/Qualifiers				
	1..20				
	/organism="unknown"				
BASE COUNT	1 a	8 c	2 g	9 t	
ORIGIN					
Query Match	0.5%; Score 20; DB 6; Length 20;				
Best Local Similarity	100.0%; Pred. No. 39;				
Matches	20; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
QY	1230	GAAAGCGAAGTGGCAGAGG	1249		
Db	20	GAAAGCGAAGTGGCAGAGG	1		
RESULT 10					
LOCUS	AR095074	20 bp	DNA	linear	PAT 08-SEP-2000
DEFINITION	Sequence 27 from patent US 6001992.				
ACCESSION	AR095074				
VERSION	AR095074.1	GI:10022599			
KEYWORDS					
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 20)				
TITLE	Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.				
JOURNAL	Antisense modulation of novel anti-apoptotic bcl-2-related proteins				
FEATURES	Patent: US 6001992-A 27 14-DEC-1999;				
	Location/Qualifiers				
	1..20				
	/organism="unknown"				
BASE COUNT	4 a	6 c	4 g	6 t	
ORIGIN					
Query Match	0.5%; Score 20; DB 6; Length 20;				
Best Local Similarity	100.0%; Pred. No. 39;				
Matches	20; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
OY	1519	AAGATGCCAGTGCCTGTG	1538		
Db	20	AAGATGCCAGTGCCTGTG	1		
RESULT 11					
LOCUS	AR095075	20 bp	DNA	linear	PAT 08-SEP-2000
DEFINITION	Sequence 28 from patent US 6001992.				
ACCESSION	AR095075				
VERSION	AR095075.1	GI:10022601			
KEYWORDS					
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 20)				
TITLE	Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.				
JOURNAL	Antisense modulation of novel anti-apoptotic bcl-2-related proteins				
FEATURES	Patent: US 6001992-A 28 14-DEC-1999;				
	Location/Qualifiers				
	1..20				
	/organism="unknown"				

BASE COUNT 9 a 5 c 4 g 2 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1676 GGCTTGATTCATGATTCCT 1695
DB 20 GGCTTGATTCATGATTCCT 1

RESULT 12

AR095076/c 20 bp DNA linear PAT 08-SEP-2000
LOCUS AR095076
DEFINITION Sequence 29 from patent US 6001992.
ACCESSION AR095076
VERSION AR095076.1 GI:10022603
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 29 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 7 c 2 g 7 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2091 TGAACCTGGATGAGAG 2110
DB 20 TGAACCTGGATGAGAG 1

RESULT 13

AR095077/c 20 bp DNA linear PAT 08-SEP-2000
LOCUS AR095077
DEFINITION Sequence 30 from patent US 6001992.
ACCESSION AR095077
VERSION AR095077.1 GI:10022605
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 30 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 8 a 3 c 6 g 3 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2231 TGAGTCTTCATTTGACC 2250
DB 20 TGAGTCTTCATTTGACC 1

RESULT 14

AR095078/c 20 bp DNA linear PAT 08-SEP-2000
LOCUS AR095078

DEFINITION Sequence 31 from patent US 6001992.
ACCESSION AR095078
VERSION AR095078.1 GI:10022607
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 31 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 5 a 9 c 1 g 5 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2366 GGCTGATGAGAGACATTTG 2385
DB 20 GGCTGATGAGAGACATTTG 1

RESULT 15

AR095079/c 20 bp DNA linear PAT 08-SEP-2000
LOCUS AR095079
DEFINITION Sequence 32 from patent US 6001992.
ACCESSION AR095079
VERSION AR095079.1 GI:10022609
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 20)
AUTHORS Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL Patent: US 6001992-A 32 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 9 a 5 c 3 g 3 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2564 GCATTGGCATCTTTGATT 2583
DB 20 GCATTGGCATCTTTGATT 1

Search completed: March 14, 2003, 07:13:19
Job time : 6854.2 secs

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 03:41:43 ; Search time 575.829 seconds

(without alignments)
15385.391 Million cell updates/sec

Title: US-09-869-894-18

Sequence: 1 tccagtaaggagtcg99gtc.....aactcttatcaataaa 3934

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	30	0.8	30	22	AAD06442 Human Mcl-1 DNA ex
C 2	21	0.5	21	16	AA03164 Human Mcl-1 gene f
C 3	21	0.5	21	22	AA26538 PCR primer p12. S
C 4	21	0.5	21	20	AA26539 PCR primer p13. S
C 5	21	0.5	21	22	AAD06439 Human Mcl-1 CDNA a
C 6	21	0.5	21	22	AAD06441 Human Mcl-1 CDNA a
C 7	20	0.5	20	16	AA03166 Human Mcl-1 gene r
C 8	20	0.5	20	21	AA239083 Human Mcl-1 anti-a
C 9	20	0.5	20	21	AA239084 Human mcl-1 anti-a

C 10	20	0.5	20	21	AA239085 Human mcl-1 anti-a
C 11	20	0.5	20	21	AA239086 Human mcl-1 anti-a
C 12	20	0.5	20	21	AA239087 Human mcl-1 anti-a
C 13	20	0.5	20	21	AA239090 Human mcl-1 anti-a
C 14	20	0.5	20	21	AA239091 Human mcl-1 anti-a
C 15	20	0.5	20	21	AA239092 Human mcl-1 anti-a
C 16	20	0.5	20	21	AA239093 Human mcl-1 anti-a
C 17	20	0.5	20	21	AA239094 Human mcl-1 anti-a
C 18	20	0.5	20	21	AA239095 Human mcl-1 anti-a
C 19	20	0.5	20	21	AA239096 Human mcl-1 anti-a
C 20	20	0.5	20	21	AA239097 Human mcl-1 anti-a
C 21	20	0.5	20	21	AA239098 Human mcl-1 anti-a
C 22	20	0.5	20	21	AA239099 Human mcl-1 anti-a
C 23	20	0.5	20	21	AA239100 Human mcl-1 anti-a
C 24	20	0.5	20	21	AA239101 Human mcl-1 anti-a
C 25	20	0.5	20	21	AA239102 Human mcl-1 anti-a
C 26	20	0.5	20	21	AA239103 Human mcl-1 anti-a
C 27	20	0.5	20	21	AA239104 Human mcl-1 anti-a
C 28	20	0.5	20	22	AAH76277 Human myeloid leuk
C 29	20	0.5	20	22	AAH76278 Human Mcl-1 CDNA a
C 30	20	0.5	20	22	AAD06437 Human Mcl-1 CDNA a
C 31	20	0.5	20	22	AAD06438 Human Mcl-1 CDNA a
C 32	20	0.5	20	22	AAD06440 Gnt-IV CDNA contai
C 33	20	0.5	39	19	AAV39021 erb B2/new promote
C 34	18	0.5	28	14	AA041910 Guanosine rich oli
C 35	18	0.5	29	21	AA063575 PCR primer used to
C 36	18	0.5	29	21	AA063576 PCR primer used to
C 37	18	0.5	38	19	AAV16068 Murine Srv gene PC
C 38	18	0.5	38	21	AA05350 Murine B2/new prome
C 39	18	0.5	38	21	AA043365 Sequence of synthe
C 40	18	0.5	41	14	AA055568 triple helix-formi
C 41	18	0.5	41	15	AA055567 Neisseria meningit
C 42	18	0.5	41	15	N. meningitidis fu
C 43	18	0.5	41	15	
C 44	18	0.5	44	22	
C 45	18	0.5	44	22	

ALIGNMENTS

RESULT 1
AAD06442/c
AAD06442 standard; DNA: 30 BP.
ID
AAD06442:
AC
AC
XX
XX
DT
DT
XX
XX
DE
DE
Human Mcl-1 DNA extending PCR primer. #105C.
XX
XX
Human; Mcl-1 gene regulatory element; Mcl-1s/deltaTM variant;
XX
XX
neutonal cell; tumour cell; apoptosis; therapy; cancer; psoriasis;
XX
XX
diabetic retinopathy; corneal graft neovascularisation;
XX
XX
neovascular glaucoma; epithelial condition; autoimmune disease;
XX
XX
rheumatoid arthritis; systemic lupus erythematosus;
XX
XX
neurodegenerative disease; PCR primer; ss.
XX
XX
Homo sapiens.
XX
XX
WO200136594-A1.
XX
XX
25-MAY-2001.
XX
XX
14-JAN-2000; 2000MO-US00969.
XX
XX
16-NOV-1999; 99US-0166113.
XX
XX
(DART-) DARTMOUTH COLLEGE.
XX
XX
Craig RW, Bingle CD, Whyte M:
XX
XX
WPI; 2001-343812/36.

XX Novel Mcl-1 gene regulatory elements, useful for modulating expression
 PT of Mcl-1 polypeptide or its variant which regulate apoptosis in
 PT neuronal or tumor cells -

XX Example 2; Page 76; 125pp; English.

XX The present invention relates to Mcl-1 gene regulatory elements and the
 CC variant Mcl-1s/deltaT_{ATM}. The anti-apoptotic Mcl-1 protein is encoded by
 CC exons 1, 2 and 3. The pro-apoptotic Mcl-1s/deltaT_{ATM} variant encoded by
 CC exons 1 and 3 is obtained due to alternative mRNA splicing. The Mcl-1
 CC gene regulatory element is useful for modulating the Mcl-1 gene
 CC expression in a cell e.g., neuronal cell or tumour cell, such that
 CC apoptosis of the cell is induced or cell viability is increased. The
 CC Mcl-1 and its regulatory elements are used for treating pathological
 CC conditions which include cancer, diabetic retinopathy, corneal graft
 CC neovascularisation and neovascular glaucoma, epithelial conditions such
 CC as psoriasis, autoimmune diseases like rheumatoid arthritis, systemic
 CC lupus erythematosus, and neurodegenerative diseases. The present sequence
 CC is a PCR primer #105C, used for the extension reaction of the human
 CC Mcl-1 DNA.

XX Sequence 30 BP; 7 A; 9 C; 8 G; 6 T; 0 other;

Query Match 0.8%; Score 30; DB 22; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00072; Mismatches 0; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 83 CGGTATCGAGTCACTACTGTCGGG 112

DB 30 CGGTATCGAGTCACTACTGTCGGG 1

RESULT 2

AAT03164/c

ID AAT03164 standard; DNA; 21 BP.

XX AAT03164;

DT 05-JUN-1996 (first entry)

XX Human Mcl-1 gene first strand primer.

XX Mcl-1; Bax; apoptosis; cell death; regulation; Bcl-2; novel;
 detection; ss.

XX Synthetic.

XX W09528497-AL.

XX 26-OCT-1995.

XX 12-APR-1995; 95WO-US04600.

XX 13-APR-1994; 94US-0226876.

XX (LJOL-) LA JOLLA CANCER RES. FOUND.

XX Reed JC, Sato T;

XX WPI; 1995-373811/48.

XX Detection of novel proteins involved in apoptosis - by interaction
 PT with proteins involved in apoptosis

XX Example 1; Page 22; 62pp; English.

XX AAT03164-T031366 are primers used for the amplification of the human
 CC Mcl-1 gene. The Mcl-1 protein is a Bcl-2 related protein, the Mcl-1
 CC protein was expressed and used to investigate the interactions of
 CC Mcl-1 with other proteins known to be involved in apoptosis
 CC (excluding the Bax protein). Proteins detected using this method can
 CC act as upstream activators or downstream effectors of a cellular

CC protein such as Bax which induces apoptosis. If the protein is a
 CC Bcl-2 related protein apoptosis levels are decreased due to the
 CC protein binding to and inactivating Bax.

XX Sequence 21 BP; 4 A; 8 C; 2 G; 7 T; 0 other;

Query Match 0.5%; Score 21; DB 16; Length 21;

Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;

07 1235 GCAGTGGCAAGAGATTATG 1255

DB 21 GCAGTGGCAAGAGATTATG 1

RESULT 3

AXX26538

ID AXX26538 standard; DNA; 21 BP.

XX AAX26538;

DT 27-MAY-1999 (first entry)

XX PCR primer P12.

XX DNA amplification; nucleotide analogue; PCR primer; ss.

XX Synthetic.

XX W09909213-AL.

XX 25-FEB-1999.

XX 10-AUG-1998; 98WO-JP03566.

XX 21-OCT-1997; 97JP-0305016.

XX 14-AUG-1997; 97JP-0231885.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Hino F, Kato I, Mukai H, Yamamoto J;

XX WPI; 1999-161059/15.

XX Simple and accurate method for DNA amplification - uses
 PT amplification in the presence of nucleotide analogues together with
 PT a compound which lowers the Tm of double-stranded nucleic acids

XX Example 6; Page 31; 36pp; Japanese.

XX PCR primers AAX26538-39 were used to exemplify the invention. The
 CC specific DNA containing nucleotide analogues is amplified in
 CC template DNA containing nucleotide analogues and a substance which lowers
 CC the Tm value of double-stranded nucleic acids. Suitable nucleotide
 CC analogues are 7-deaza-dGTP, 7-deaza-dATP, dITP and hydroxymethyl-dUTP.
 CC Suitable Tm value-lowering substances are formamide, dimethyl sulfoxide
 CC and trimethylglycine. The methods improve the amplification of DNA.
 CC Also, DNA fragments which originated as RNA can be amplified without
 CC purifying the RNAs in sample.

XX Sequence 21 BP; 4 A; 5 C; 7 G; 5 T; 0 other;

Query Match 0.5%; Score 21; DB 20; Length 21;

Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;

07 586 CGCAGTGCCTGGAGATTATC 606

DB 1 CGCAGTGCCTGGAGATTATC 21

RESULT 4


```

AAx26539/c
ID  AAX26539 standard; DNA: 21 BP.
XX
XX  AAX26539;
XX
XX  27-MAY-1999 (first entry)
XX
XX  PCR primer PJ3.
XX
XX  DNA amplification; nucleotide analogue; PCR primer; ss.
XX
XX  Synthetic.
XX
XX  WO9909213-AL.
XX
XX  25-FEB-1999.
XX
XX  10-AUG-1998; 98WO-JP03566.
XX
XX  21-OCT-1997; 97JP-0305016.
XX
XX  14-AUG-1997; 97JP-0231885.
XX
XX  (TAKI ) TAKARA SHUZO CO LTD.
XX
XX  Hino F, Kato I, Mukai H, Yamamoto J;
XX
XX  WPI; 1999-181059/15.
XX
XX  Simple and accurate method for DNA amplification - uses
XX  amplification in the presence of nucleotide analogues together with
XX  a compound which lowers the Tm of double-stranded nucleic acids
XX
XX  Example 6; Page 31; 36pp; Japanese.
XX
XX  PCR primers AAX26538-39 were used to exemplify the invention. The
XX  specification describes methods for DNA amplification, wherein a
XX  template DNA containing nucleotide analogues is amplified in
XX  the presence of nucleotide analogues and a substance which lowers
XX  the Tm value of double-stranded nucleic acids. Suitable nucleotide
XX  analogues are 7-deaza-dGTP, 7-deaza-dATP, dTTP and hydroxymethyl-dTTP.
XX  Suitable Tm value-lowering substances are formamide, dimethyl sulfoxide
XX  and trimethylglycine. The methods improve the amplification of DNA.
XX  Also, DNA fragments which originated as RNA can be amplified without
XX  purifying the RNAs in sample.
XX
XX  Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 other;
XX
XX  Query Match 0.5%; Score 21; Length 21;
XX  Best Local Similarity 100.0%; Pred. No. 17;
XX  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1014 CTTCCATGTAGAGGACTTACA 1034
XX  DB 21 CTTCCATGTAGAGGACTTACA 1
XX
XX  RESULT 5
XX  AAD06439
XX  ID AAD06439 standard; DNA: 21 BP.
XX
XX  AAD06439;
XX
XX  10-AUG-2001 (first entry)
XX
XX  Human Mcl-1 cDNA amplifying RT-PCR primer, Mcl-1-F5.
XX
XX  Human; Mcl-1 gene regulatory element; Mcl-1s/deltaTM variant;
XX  neuronal cell; tumour cell; apoptosis; therapy; cancer; psoriasis;
XX  diabetic retinopathy; corneal graft neovascularisation;
XX  neovascular glaucoma; epithelial condition; autoimmune disease;
XX  rheumatoid arthritis; systemic lupus erythematosus;
XX  neurodegenerative disease; PCR primer; ss.
XX

```

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OS Homo sapiens.
XX
XX  WO200136594-AL.
XX
XX  25-MAY-2001.
XX
XX  14-JAN-2000; 2000MO-US00969.
XX
XX  16-NOV-1999; 99US-0166113.
XX
XX  (DART-) DARTMOUTH COLLEGE.
XX
XX  Craig RW, Bingle CD, Whyte M;
XX
XX  WPI; 2001-343812/36.
XX
XX  Novel Mcl-1 gene regulatory elements, useful for modulating expression
XX  of Mcl-1 polypeptide or its variant which regulate apoptosis in
XX  neuronal or tumor cells -
XX
XX  Example 2; Page 75; 125pp; English.
XX
XX  The present invention relates to Mcl-1 gene regulatory elements and the
XX  variant Mcl-1s/deltaTM. The anti-apoptotic Mcl-1 protein is encoded by
XX  exons 1, 2 and 3. The pro-apoptotic Mcl-1s/deltaTM variant encoded by
XX  exons 1 and 3 is obtained due to alternative mRNA splicing. The Mcl-1
XX  gene regulatory element is useful for modulating the Mcl-1 gene
XX  expression in a cell e.g., neuronal cell or tumour cell, such that
XX  apoptosis of the cell is induced or cell viability is increased. The
XX  Mcl-1 and its regulatory elements are used for treating pathological
XX  conditions which include cancer, diabetic retinopathy, corneal graft
XX  neovascularisation and neovascular glaucoma, epithelial conditions such
XX  as psoriasis, autoimmune diseases like rheumatoid arthritis, systemic
XX  lupus erythematosus, and neurodegenerative diseases. The present sequence
XX  is a RT-PCR primer Mcl-1-F5, used for the amplification of the human
XX  Mcl-1 cDNA.
XX
XX  Sequence 21 BP; 3 A; 5 C; 8 G; 5 T; 0 other;
XX
XX  Query Match 0.5%; Score 21; DB 22; Length 21;
XX  Best Local Similarity 100.0%; Pred. No. 17;
XX  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 5 GTAAGGAGTCGGGCTCTTCCC 25
XX  DB 1 GTAAGGAGTCGGGCTCTTCCC 21
XX
XX  RESULT 6
XX  AAD06441/c
XX  ID AAD06441 standard; DNA: 21 BP.
XX
XX  AAD06441;
XX
XX  10-AUG-2001 (first entry)
XX
XX  Human Mcl-1 cDNA amplifying RT-PCR primer, Mcl-1-R7.
XX
XX  Human; Mcl-1 gene regulatory element; Mcl-1s/deltaTM variant;
XX  neuronal cell; tumour cell; apoptosis; therapy; cancer; psoriasis;
XX  diabetic retinopathy; corneal graft neovascularisation;
XX  neovascular glaucoma; epithelial condition; autoimmune disease;
XX  rheumatoid arthritis; systemic lupus erythematosus;
XX  neurodegenerative disease; PCR primer; ss.
XX
XX  Homo sapiens.
XX
XX  WO200136594-AL.
XX
XX  25-MAY-2001.
XX
XX  14-JAN-2000; 2000MO-US00969.
XX

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```
PR 16-NOV-1999; 9905-0166113.
XX
XX (DART-) DARTMOUTH COLLEGE.
PA
XX Craig RW, Bangle CD, Whyte M;
PI
XX WPI; 2001-343812/36.
XX
XX Novel Mcl-1 gene regulatory elements, useful for modulating expression
PT of Mcl-1 polypeptide or its variant which regulate apoptosis in
PT neuronal or tumor cells -
XX
XX Example 2; Page 75; 125pp; English.
XX
XX The present invention relates to Mcl-1 gene regulatory elements and the
CC variant Mcl-1s/deltaarm. The anti-apoptotic Mcl-1 protein is encoded by
CC exons 1, 2 and 3. The pro-apoptotic Mcl-1s/deltaarm variant encoded by
CC exons 1 and 3 is obtained due to alternative mRNA splicing. The Mcl-1
CC gene regulatory element is useful for modulating the Mcl-1 gene
CC expression in a cell e.g., neuronal cell or tumor cell, such that
CC apoptosis of the cell is induced or cell viability is increased. The
CC Mcl-1 and its regulatory elements are used for treating pathological
CC conditions which include cancer, diabetic retinopathy, corneal graft
CC neovascularisation and neovascular glaucoma, epithelial conditions such
CC as psoriasis, autoimmune diseases like rheumatoid arthritis, systemic
CC lupus erythematosus, and neurodegenerative diseases. The present sequence
CC is a RT-PCR primer Mcl-1-R7, used for the amplification of the human
CC Mcl-1 cDNA.
XX
XX Sequence 21 BP; 1 A; 8 C; 2 G; 10 T; 0 other;
SQ
XX
XX Query Match 0.5%; Score 21; DB 22; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1230 GAAAGCAAGTGCAGAGAGA 1250
XX |||||||||||||||
XX 21 GAAAGCAAGTGCAGAGAGA 1
DB
XX
XX RESULT 7
XX AAT03166/c
XX ID AAT03166 standard; DNA; 20 BP.
XX
XX AAT03166;
AC
XX 05-JUN-1996 (first entry)
DT
XX Human Mcl-1 gene reverse PCR primer.
DE
XX Mcl-1; Bax; apoptosis; cell death; regulation; Bcl-2; novel;
KM detection; ss.
XX
XX Synthetic.
OS
XX W09528497-A1.
PN
XX 26-OCT-1995.
PD
XX
XX 12-APR-1995; 95MO-US04600.
PE
XX 13-APR-1994; 94US-0226876.
PR
XX (LJOL-) LA JOLLA CANCER RES FOUND.
PA
XX Reed JC, Sato T;
PI
XX WPI; 1995-373811/48.
XX
XX Detection of novel proteins involved in apoptosis - by interaction
PT with proteins involved in apoptosis
PT
XX Example 1; Page 23; 62pp; English.
XX
```

```
XX
XX AAT03164-T031366 are primers used for the amplification of the human
CC Mcl-1 gene. The Mcl-1 protein is a Bcl-2 related protein, the Mcl-1
CC protein was expressed and used to investigate the interactions of
CC Mcl-1 with other proteins known to be involved in apoptosis
CC (excluding the Bax protein). Proteins detected using this method can
CC act as upstream activators or downstream effectors of a cellular
CC protein such as Bax which induces apoptosis. If the protein is a
CC Bcl-2 related protein apoptosis levels are decreased due to the
CC protein binding to and inactivating Bax.
XX
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;
SQ
XX
XX Query Match 0.5%; Score 20; DB 16; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 51;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1182 GGACTCCAGCTGTACTTC 1201
XX |||||||||||||||
XX 20 GGACTCCAGCTGTACTTC 1
DB
XX
XX RESULT 8
XX AAZ39083/c
XX ID AAZ39083 standard; DNA; 20 BP.
XX
XX AAZ39083;
AC
XX 29-FEB-2000 (first entry)
DT
XX Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20407.
DE
XX
XX Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
KW inflammation; diagnosis; phosphorothioate; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX US6001992-A.
PN
XX 14-DEC-1999.
PD
XX 07-JAN-1999; 99US-0226568.
PF
XX 07-JAN-1999; 99US-0226568.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX WPI; 2000-061908/05.
XX
XX Antisense oligonucleotides which modulate the expression of novel
PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
PT and treating associated diseases e.g. cancer -
XX
XX Claim 31; Column 33; 28pp; English.
PS
XX
XX The present invention describes antisense oligonucleotides which modulate
CC the expression of novel anti-apoptotic bcl-2-related proteins. The
CC antisense oligonucleotides can be used as therapeutic agents to prevent
CC or delay inflammation or tumour formation by promoting apoptosis in
CC human cells or tissues. They can also be used as research agents to
CC establish the function of particular genes and as diagnostic agents in
CC bcl-2-related proteins in a sample. The antisense oligonucleotides
CC given in the present invention were designed to target human A1 and
CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC present sequence represents an antisense oligonucleotide for the
CC human mcl-1 nucleotide sequence.
XX
XX Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 other;
SQ
```

```

Query Match          0.5%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 501 CGGGGATCTGTAATACA 520
   |||||||
Db 20 CGGGGATCTGTAATACA 1

RESULT 9
AAZ39084/c
ID AAZ39084 standard; DNA; 20 BP.
XX
AC AAZ39084;
XX
DT 29-FEB-2000 (first entry)
XX
DE Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20408.
XX
KM Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
XX inflammation; diagnosis; phosphorothioate; ss.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN US6001992-A.
XX
PD 14-DEC-1999.
XX
PE 07-JAN-1999; 99US-0226568.
XX
PR 07-JAN-1999; 99US-0226568.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR WPI; 2000-061908/05.
XX
PT Antisense oligonucleotides which modulate the expression of novel
XX anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
XX and treating associated diseases e.g. cancer -
XX
PS Claim 31; Column 33; 28pp; English.
XX
CC The present invention describes antisense oligonucleotides which modulate
CC the expression of novel anti-apoptotic bcl-2-related proteins. The
CC antisense oligonucleotides can be used as therapeutic agents to prevent
CC or delay inflammation or tumour formation by promoting apoptosis in
CC human cells or tissues. They can also be used as research agents to
CC establish the function of particular genes and as diagnostic agents in
CC sandwich assays for detecting the level of novel anti-apoptotic
CC bcl-2-related proteins in a sample. The antisense oligonucleotides
CC given in the present invention were designed to target human A1 and
CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC present sequence represents an antisense oligonucleotide for the
CC human mcl-1 nucleotide sequence.
XX
SQ Sequence 20 BP; 0 A; 4 C; 7 G; 9 T; 0 other;

Query Match          0.5%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 636 CGCCAGGACAAAGCCAA 655
   |||||||
Db 20 CGCCAGGACAAAGCCAA 1

RESULT 10
AAZ39085/c

```

```

ID AAZ39085 standard; DNA; 20 BP.
XX
AC AAZ39085;
XX
DT 29-FEB-2000 (first entry)
XX
DE Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20416.
XX
KM Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
XX inflammation; diagnosis; phosphorothioate; ss.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN US6001992-A.
XX
PD 14-DEC-1999.
XX
PE 07-JAN-1999; 99US-0226568.
XX
PR 07-JAN-1999; 99US-0226568.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;
XX
DR WPI; 2000-061908/05.
XX
PT Antisense oligonucleotides which modulate the expression of novel
XX anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
XX and treating associated diseases e.g. cancer -
XX
PS Claim 31; Column 33; 28pp; English.
XX
CC The present invention describes antisense oligonucleotides which modulate
CC the expression of novel anti-apoptotic bcl-2-related proteins. The
CC antisense oligonucleotides can be used as therapeutic agents to prevent
CC or delay inflammation or tumour formation by promoting apoptosis in
CC human cells or tissues. They can also be used as research agents to
CC establish the function of particular genes and as diagnostic agents in
CC sandwich assays for detecting the level of novel anti-apoptotic
CC bcl-2-related proteins in a sample. The antisense oligonucleotides
CC given in the present invention were designed to target human A1 and
CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
CC present sequence represents an antisense oligonucleotide for the
CC human mcl-1 nucleotide sequence.
XX
SQ Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 other;

Query Match          0.5%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2366 GGTGATGGAGGACATTG 2385
   |||||||
Db 20 GGTGATGGAGGACATTG 1

RESULT 11
AAZ39086/c
ID AAZ39086 standard; DNA; 20 BP.
XX
AC AAZ39086;
XX
DT 29-FEB-2000 (first entry)
XX
DE Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20420.
XX
KM Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
XX inflammation; diagnosis; phosphorothioate; ss.
XX

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OS Synthetic.
OS Homo sapiens.
XX US6001992-A.
XX 14-DEC-1999.
XX 07-JAN-1999; 99US-0226568.
XX 07-JAN-1999; 99US-0226568.
XX (ISIS-) ISIS PHARM INC.
XX Ackermann EJ, Marcussen EG, Bennett CF, Dean NM;
XX WPI: 2000-061908/05.
XX
XX Antisense oligonucleotides which modulate the expression of novel
XX anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
XX and treating associated diseases e.g. cancer -
XX
XX Claim 31; Column 33; 28pp; English.
XX
XX The present invention describes antisense oligonucleotides which modulate
XX the expression of novel anti-apoptotic bcl-2-related proteins. The
XX antisense oligonucleotides can be used as therapeutic agents to prevent
XX or delay inflammation or tumour formation by promoting apoptosis in
XX human cells or tissues. They can also be used as research agents to
XX establish the function of particular genes and as diagnostic agents in
XX sandwich assays for detecting the level of novel anti-apoptotic
XX bcl-2-related proteins in a sample. The antisense oligonucleotides
XX given in the present invention were designed to target human A1 and
XX mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
XX present sequence represents an antisense oligonucleotide for the
XX human mcl-1 nucleotide sequence.
XX
XX Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 other;
SQ
XX
XX Query Match 0.5%; Score 20; DB 21; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 51;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3207 TGTATGGGAGAGAACTGCC 3226
DB 20 TGTATGGGAGAGAACTGCC 1
XX
XX RESULT 12
XX AA239087/C
XX ID AA239087 standard; DNA; 20 BP.
XX
XX AA239087;
XX
XX 29-FEB-2000 (first entry)
XX
XX Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20421.
XX
XX Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
XX mcl-1; apoptosis; cancer; antiinflammatory; cyostatic; tumour;
XX inflammation; diagnosis; phosphorothioate; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX US6001992-A.
XX
XX 14-DEC-1999.
XX
XX 07-JAN-1999; 99US-0226568.
XX
XX 07-JAN-1999; 99US-0226568.
XX
XX (ISIS-) ISIS PHARM INC.
XX

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XX
XX Ackermann EJ, Marcussen EG, Bennett CF, Dean NM;
XX WPI: 2000-061908/05.
XX
XX Antisense oligonucleotides which modulate the expression of novel
XX anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
XX and treating associated diseases e.g. cancer -
XX
XX Claim 31; Column 33; 28pp; English.
XX
XX The present invention describes antisense oligonucleotides which modulate
XX the expression of novel anti-apoptotic bcl-2-related proteins. The
XX antisense oligonucleotides can be used as therapeutic agents to prevent
XX or delay inflammation or tumour formation by promoting apoptosis in
XX human cells or tissues. They can also be used as research agents to
XX establish the function of particular genes and as diagnostic agents in
XX sandwich assays for detecting the level of novel anti-apoptotic
XX bcl-2-related proteins in a sample. The antisense oligonucleotides
XX given in the present invention were designed to target human A1 and
XX mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
XX present sequence represents an antisense oligonucleotide for the
XX human mcl-1 nucleotide sequence.
XX
XX Sequence 20 BP; 5 A; 3 C; 5 G; 7 T; 0 other;
SQ
XX
XX Query Match 0.5%; Score 20; DB 21; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 51;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3391 TAAAGCTGTCGTGCCAAT 3410
DB 20 TAAAGCTGTCGTGCCAAT 1
XX
XX RESULT 13
XX AA239090/C
XX ID AA239090 standard; DNA; 20 BP.
XX
XX AA239090;
XX
XX 29-FEB-2000 (first entry)
XX
XX Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20404.
XX
XX Human; A1; anti-apoptotic; bcl-2-related protein; antisense inhibition;
XX mcl-1; apoptosis; cancer; antiinflammatory; cyostatic; tumour;
XX inflammation; diagnosis; phosphorothioate; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX US6001992-A.
XX
XX 14-DEC-1999.
XX
XX 07-JAN-1999; 99US-0226568.
XX
XX 07-JAN-1999; 99US-0226568.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ackermann EJ, Marcussen EG, Bennett CF, Dean NM;
XX WPI: 2000-061908/05.
XX
XX Antisense oligonucleotides which modulate the expression of novel
XX anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
XX and treating associated diseases e.g. cancer -
XX
XX Example 12; Column 33; 28pp; English.
XX
XX The present invention describes antisense oligonucleotides which modulate
XX

```

CC the expression of novel anti-apoptotic bcl-2-related proteins. The
 CC antisense oligonucleotides can be used as therapeutic agents to prevent
 CC or delay inflammation or tumour formation by promoting apoptosis in
 CC human cells or tissues. They can also be used as diagnostic agents to
 CC establish the function of particular genes and as diagnostic agents in
 CC sandwich assays for detecting the level of novel anti-apoptotic
 CC bcl-2-related proteins in a sample. The antisense oligonucleotides
 CC given in the present invention were designed to target human Al and
 CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
 CC present sequence represents an antisense oligonucleotide for the
 CC human mcl-1 nucleotide sequence.

XX Sequence 20 BP; 5 A; 8 C; 4 G; 3 T; 0 other;

Query Match 0.5%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 50 GGGAGCTGGCATGTTGGC 69
 Db 20 GGGAGCTGGCATGTTGGC 1

RESULT 14

AA239091/c
 ID AA239091 standard; DNA; 20 BP.

AC AA239091;

DT 29-FEB-2000 (first entry)

XX Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20405.

DE Human; Al; anti-apoptotic; bcl-2-related protein; antisense inhibition;
 KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
 KM inflammation; diagnosis; phosphorothioate; ss.

OS Synthetic.

OS Homo sapiens.

XX US6001992-A.

PN 14-DEC-1999.

PD 07-JAN-1999; 99US-0226568.

PR 07-JAN-1999; 99US-0226568.

PA (ISIS-) ISIS PHARM INC.

PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;

DR WPI; 2000-061908/05.

XX Antisense oligonucleotides which modulate the expression of novel
 PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
 PT and treating associated diseases e.g. cancer -
 XX Example 12; Column 33; 28pp; English.

CC The present invention describes antisense oligonucleotides which modulate
 CC the expression of novel anti-apoptotic bcl-2-related proteins. The
 CC antisense oligonucleotides can be used as therapeutic agents to prevent
 CC or delay inflammation or tumour formation by promoting apoptosis in
 CC human cells or tissues. They can also be used as research agents to
 CC establish the function of particular genes and as diagnostic agents in
 CC sandwich assays for detecting the level of novel anti-apoptotic
 CC bcl-2-related proteins in a sample. The antisense oligonucleotides
 CC given in the present invention were designed to target human Al and
 CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
 CC present sequence represents an antisense oligonucleotide for the
 CC human mcl-1 nucleotide sequence.

SQ Sequence 20 BP; 5 A; 9 C; 4 G; 2 T; 0 other;

Query Match 0.5%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 152 CGGAGGGCGCATGTTGGCT 171
 Db 20 CGGAGGGCGCATGTTGGCT 1

RESULT 15

AA239092/c
 ID AA239092 standard; DNA; 20 BP.

AC AA239092;

DT 29-FEB-2000 (first entry)

XX Human mcl-1 anti-apoptotic bcl-2-related protein antisense oligo #20406.

DE Human; Al; anti-apoptotic; bcl-2-related protein; antisense inhibition;
 KW mcl-1; apoptosis; cancer; antiinflammatory; cytostatic; tumour;
 KM inflammation; diagnosis; phosphorothioate; ss.

OS Synthetic.

OS Homo sapiens.

PN US6001992-A.

PD 14-DEC-1999.

PT 07-JAN-1999; 99US-0226568.

PR 07-JAN-1999; 99US-0226568.

PA (ISIS-) ISIS PHARM INC.

PI Ackermann EJ, Marcusson EG, Bennett CF, Dean NM;

DR WPI; 2000-061908/05.

XX Antisense oligonucleotides which modulate the expression of novel
 PT anti-apoptotic bcl-2-related proteins are useful for inducing apoptosis
 PT and treating associated diseases e.g. cancer -
 XX Example 12; Column 33; 28pp; English.

CC The present invention describes antisense oligonucleotides which modulate
 CC the expression of novel anti-apoptotic bcl-2-related proteins. The
 CC antisense oligonucleotides can be used as therapeutic agents to prevent
 CC or delay inflammation or tumour formation by promoting apoptosis in
 CC human cells or tissues. They can also be used as research agents to
 CC establish the function of particular genes and as diagnostic agents in
 CC sandwich assays for detecting the level of novel anti-apoptotic
 CC bcl-2-related proteins in a sample. The antisense oligonucleotides
 CC given in the present invention were designed to target human Al and
 CC mcl-1 anti-apoptotic bcl-2-related protein nucleotide sequences. The
 CC present sequence represents an antisense oligonucleotide for the
 CC human mcl-1 nucleotide sequence.

SQ Sequence 20 BP; 2 A; 10 C; 3 G; 5 T; 0 other;

Query Match 0.5%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 20 AGGAGCTGGAGCGGTRACAG 1

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Fri Mar 14 14:08:31 2003

us-09-869-894-18.olszlm50.rng

Page 8

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 04:32:49 ; Search time 732.181 seconds
(Without alignments)

17253.226 Million cell updates/sec

Title: US-09-869-894-1

Perfect score: 780
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database :

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- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
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- 6: em_estpl:*
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- 11: qb_hic:*
- 12: qb_est3:*
- 13: qb_est4:*
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- 15: em_estfun:*
- 16: em_estom:*
- 17: qb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_huv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
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- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	28	3.6	43	9	A1370619
C 2	16	2.1	46	17	BH635174
C 3	15	1.9	43	14	C01095
C 4	14	1.8	26	17	A2439313
C 5	13	1.7	25	17	BH855488
C 6	13	1.7	25	17	TA23508P

Result No.	Score	Query Match	Length DB	ID	Description
C 7	13	1.7	26	17	A2787019
C 8	9	1.3	29	17	A2323085
C 9	13	1.7	30	17	AL761633
C 10	13	1.7	31	17	A2809484
C 11	13	1.7	33	9	A240558
C 12	13	1.7	35	9	A0009945
C 13	13	1.7	36	17	A2482026
C 14	13	1.7	36	17	BH849581
C 15	13	1.7	38	17	AL762626
C 16	13	1.7	40	17	BH011458
C 17	13	1.7	43	9	AA235295
C 18	13	1.7	43	17	BH792796
C 19	13	1.7	45	17	A2389050
C 20	13	1.7	46	9	AA920919
C 21	13	1.7	46	14	N70117
C 22	13	1.7	47	14	C00031
C 23	13	1.7	48	17	A2946920
C 24	13	1.7	50	9	AU104419
C 25	13	1.7	50	14	BM733456
C 26	13	1.5	19	17	A2346703
C 27	12	1.5	21	17	A2508359
C 28	12	1.5	21	17	A2816467
C 29	12	1.5	22	17	A2786328
C 30	12	1.5	23	17	A2462638
C 31	12	1.5	24	9	A0260073
C 32	12	1.5	25	17	A2845871
C 33	12	1.5	26	17	BH754276
C 34	12	1.5	27	13	BM395315
C 35	12	1.5	28	9	AT153397
C 36	12	1.5	29	14	D45819
C 37	12	1.5	30	9	AU257038
C 38	12	1.5	30	9	AU259737
C 39	12	1.5	30	10	AW332749
C 40	12	1.5	30	17	A2346753
C 41	12	1.5	31	17	BH863143
C 42	12	1.5	32	9	AU254252
C 43	12	1.5	32	17	A2331642
C 44	12	1.5	32	17	A2469379
C 45	12	1.5	32	17	A2663912

ALIGNMENTS

RESULT 1
LOCUS A1370619/C
DEFINITION ta40f05.x1 Soares total fetus NB2HP8.9w Homo sapiens cDNA clone IMAGE:2046561.3' similar to SW-BFL1 HUMAN O16548 BC12-RELATED PROTEIN A1, contains element TAR1 repetitive element ;, mRNA

ACCESSION A1370619
VERSION A1370619.1 GI:4149372
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 43)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 431 std Error: 0.00
Seq primer: -40up from Gibco

FEATURES
source location/Qualifiers
1..43

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Query Match: 3.6%; score 28; DB 9; Length 43;
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 526 CCGAAATCGCTCGATGACTTTTTCAG 533
      |||||||
Db 28 CCGAAATCGCTCGATGACTTTTTCAG 1

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FEATURES
source

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location/Qualifiers
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/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescuenMu (engineered from
pBluescript backbone); Site_1: BamHI; Site_2: BglII;
RescuenMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
sites. For more information on RescuenMu, go to the web
site www.zmnh.ias.utcd.edu and follow the links for
RescuenMu. Grid I was grown at Berkeley in 2001. DNA wasm

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	DB	24	TGAATTGGATATT	39	
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	Best Local Similarity				100.0%; Pred. No. 1.3e+03;
	Matches 16; Conservative				0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"
/note="Organ: blood; Vector: 1-9t-11; Site: 1: Eco-RI;
Monocytes were prepared from blood by ficoll-hypaque,
percoll and 1 cell resecting purification steps (purity:
96 %). mRNA was prepared from activated monocytes from a
patient with rheumatoid arthritis. mRNA was reverse
transcribed with MuLV. Using Eco-RI linkers cDNA was
cloned into 1-9t-11 vector arms. The cDNA library was
screened by differential hybridization using radioactively
labeled ss-cDNA from activated and non-activated
monocytes."
BASE COUNT      15 a      9 c      4 g      15 t
ORIGIN
Query Match      1.9%; Score 15; DB 14; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      496 TGGGAATAAGCGTTT 510
|||||
Db      42 TGGGAATAAGCGTTT 28

```


AZ439313 26 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION IM022920R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M022920 R, DNA sequence.
 ACCESSION AZ439313
 VERSION
 KEYWORDS
 SOURCE house mouse
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 26)
 REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0229 row: j column: 20
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
 1..26
 /organism="Mus musculus"
 /strain="C57Bl/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M022920"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; purified genomic DNA from M.
 musculus C57Bl/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1|4732114|gbl|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BH855488 25 bp DNA linear GSS 08-JUL-2002
 LOCUS
 DEFINITION SALK_085052.22.25.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_085052.22.25.x, DNA
 sequence.
 ACCESSION BH855488
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 25)
 REFERENCE
 AUTHORS Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,
 C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 TITLE Unpublished (2001)
 JOURNAL
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (Signal)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1..25
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_085052.22.25.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 6 a 1 c 5 g 13 t
 ORIGIN
 Query Match 1.7%; Score 13; DB 17; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.1e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 760 AATTGTATGAT 772
 Db 12 AATTGTATGAT 24

RESULT 6
 TA23F08P/c 25 bp DNA linear GSS 13-DEC-2000
 LOCUS
 DEFINITION T. brucei sheared genomic DNA clone 23f08, forward sequence,
 genomic survey sequence.
 ACCESSION AL453160
 VERSION AL453160.1 GI:11847458
 KEYWORDS
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 25)
 REFERENCE Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-sayed,N., Hou,L.,
 Weillie,S.E., Rajandream,W.A. and Barrell,B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

BASE COUNT 12 a 5 c 2 g 7 t
 ORIGIN
 Query Match 1.8%; Score 14; DB 17; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 719 ACCCTCCAGAGTA 732
 Db 7 ACCCTCCAGAGTA 20

RESULT 5

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nhl@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_Brucei/.

FEATURES
SOURCE
1. .25
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="23f08"

BASE COUNT
ORIGIN
11 a 4 c 4 g 6 t

Query Match 1.7%; Score 13; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TATTCAACCACT 299
|||||
Db 20 TATTCAACCACT 8

RESULT 7
LOCUS A2787019 26 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0032B19 Mouse 10kb plasmid UUC1M library Mus musculus genomic
ACCESSION A2787019
VERSION A2787019.1 GI:12925362
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0032 row: B column: 19
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. .26

FEATURES
SOURCE
1. .26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0032B19"
/clone_lib="Mouse 10kb plasmid UUC1M library"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pPM42 (614732114bp/AF129072.1) a copy-number
inducible derivative of plasmid RL7 the vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.7%; Score 13; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 CCACGAGCAGAA 77
|||||
Db 4 CCACGAGCAGAA 16

RESULT 8
LOCUS A2323085 29 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0044U02F Mouse 10kb plasmid UUC1M library Mus musculus genomic
ACCESSION A2323085
VERSION A2323085.1 GI:10377460
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0044 row: J column: 02
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1. .29

FEATURES
SOURCE
1. .29
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0044U02"
/clone_lib="Mouse 10kb plasmid UUC1M library"

```
/sex="Male"  
/lab_host="E. coli strain XL10-gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g11473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-gold (Stratagene) cells  
and selected for ampicillin resistance."
```

BASE COUNT
ORIGIN 2 a 6 c 11 g 10 t

Query Match 1.7%; Score 13; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 613 AGGACACTGCATA 625

Db 22 AGGACACTGCATA 10

RESULT 9
LOCUS AL761633 30 bp DNA linear GSS 18-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-227B05-014266,
genomic survey sequence.
ACCESSION AL761633
VERSION AL761633.1 GI:21504571
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
and Weissshaar,B.
TITLE A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
JOURNAL Unpublished
AUTHORS 2
TITLES Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
JOURNAL Unpublished
AUTHORS 3 (bases 1 to 30)
TITLES Strizhov,N., Rosso,M., Li,Y. and Weissshaar,B.
Direct Submission
JOURNAL Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-Von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone MPF21. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI', information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
SOURCE 1. 30
Location/Qualifiers
/organism="Arabidopsis thaliana"

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/strain="Columbia 0"  
/db_xref="taxon:3702"  
/clone="GK-227B05-014266"  
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"  
/note="PCR was performed on DNA from Arabidopsis thaliana  
plants (T1) which were transformed with the T-DNA from  
vector pAC161. The lines contain one or more T-DNA  
insertions. The DNA fragment(s) resulting from the PCR  
were directly sequenced to determine the genomic sequence  
flanking the insertion. Sequences displaying significant  
similarity to the A. thaliana nuclear genome sequence were  
processed for submission. T-DNA derived sequences were  
removed"
```

BASE COUNT 12 a 3 c 7 g 8 t

Query Match 1.7%; Score 13; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 AAGGACTTGAA 318

Db 10 AAGGACTTGAA 22

RESULT 10
LOCUS A2809484 31 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0073F04R Mouse 10kb plasmid UNGC1M library Mus musculus genomic
clone UNGC2M0073F04 R, DNA sequence.
ACCESSION A2809484
VERSION A2809484.1 GI:12975843
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: F column: 04
Seq primer: CACACGCGAAGACCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers

FEATURES
SOURCE 1. 31
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNG2M0073F04"
/clone_lib="Mouse 10kb plasmid UNGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g147321419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 14 a 7 c 7 g 3 t

ORIGIN

Query Match 1.7%; Score 13; DB 17; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Oy 135 CGCTCTACAGATA 147
DB 4 CGCTCTACAGATA 16

RESULT 11 33 bp mRNA linear EST 15-JAN-2002
LOCUS AU240558
DEFINITION AU240558 UV irradiated OLHNI cell line cDNA library (OLC) Oryzias latipes cDNA clone OLC21.11d, mRNA sequence.
ACCESSION AU240558
VERSION AU240558.1 GI:18153137
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha; Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

REFERENCE 1 (bases 1 to 33)
AUTHORS Naruse, K., Mitani, H. and Tanaka, M.
TITLE Medaka EST Project In University of Tokyo (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Kiyoshi Naruse
Department of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-Ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4443
Fax: 81-3-5841-4410
Email: naruse@biol.s.u-tokyo.ac.jp

FEATURES
This clone was isolated from UV irradiated OLHNI cell line cDNA library (OLC) 5' end sequences.
Location/Qualifiers
1. .33
/organism="Oryzias latipes"
/strain="HN1"
/db_xref="taxon:8090"
/clone="OLC21.11d"
/clone_lib="UV irradiated OLHNI cell line cDNA library (OLC)"

BASE COUNT 10 a 9 c 5 g 8 t 1 others

ORIGIN

Query Match 1.7%; Score 13; DB 9; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 26 TCACAGCTTCAA 38
DB 16 TCACAGCTTCAA 28

RESULT 12

AU009945 35 bp mRNA linear EST 31-JUL-1998
LOCUS AU009945
DEFINITION AU009945 Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU009945
VERSION AU009945.1 GI:3346625
KEYWORDS EST.
SOURCE fission yeast.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 35)
AUTHORS Morimyo, M. and Mita, K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsunori Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-Ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
1. .35
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone="spc00705"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

BASE COUNT 19 a 2 c 6 g 8 t

ORIGIN

Query Match 1.7%; Score 13; DB 9; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 99 ATATATTACAGC 111
DB 8 ATATATTACAGC 20

RESULT 13 36 bp DNA linear GSS 04-OCT-2000
LOCUS A2482026
DEFINITION AU0306K18R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0306K18 R, DNA sequence.
ACCESSION A2482026
VERSION A2482026.1 GI:10643091
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 36)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Dival, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Research Bldg., 20 S. 2030 E., SIC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0306 row: K column: 18
 Seq primer: CACACAGGAACGATGACC
 Class: plasmid ends
 High quality sequence stop: 36.

FEATURES

source

Location/Qualifiers

1..36

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="U06C1M0306K18"

/clone_lib="Mouse 10kb plasmid U06C1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.003 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (g147321141g147329072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 6 a 4 c 16 g 10 t

ORIGIN

Query Match 1.7%; Score 13; DB 17; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.7e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 438 TTTTGTTCGGGAG 450

Db 2 TTTTGTTCGGGAG 14

RESULT 14

BH849581

LOCUS

Definition SALK_069905.21.55.x Arabidopsis thaliana T-DNA insertion lines

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 36)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

The Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 T-DNA. This sequence lies within 300 bases of the 5' end of
 At5g15570.
 Class: T-DNA tagged.

FEATURES

source

Location/Qualifiers

1..36

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_069905.21.55.x"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more T-DNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tDNA_protocols.html"

BASE COUNT 8 a 1 c 11 g 15 t 1 others

ORIGIN

Query Match 1.7%; Score 13; DB 17; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.7e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 334 TGGGAGAGATTG 346

Db 15 TGGGAGAGATTG 27

RESULT 15

AL762626

LOCUS

Definition Arabidopsis thaliana T-DNA flanking sequence GK-026F02-013759,

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

A pipeline for automated high-throughput generation of FSNs

Unpublished

2

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission

Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion close to or within gene At1g29750. The

sequences are generated at the MPI for Plant Breeding Research in

the context of the GABI-Kat Project. GABI-Kat is part of the German

Plant Genomics program designated 'GABI'. Information on line

availability can be found at:

<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

Location/Qualifiers

1..36

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"
 /clone="GK-026F02-013759"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 9 a 4 c 9 g 16 t
 ORIGIN

Query Match 1.7%; Score 13; DB 17; Length 38;
 Best Local Similarity 100.0%; Pred. No. 5.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 433 TCATATTTGTG 445
 |||||||||
 Db 7 TCATATTTGTG 19

Search completed: March 14, 2003, 08:29:33
 Job time : 738.181 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 04:33:38 ; Search time 95.137 seconds
(without alignments)
12681.353 Million cell updates/sec

Title: US-09-869-894-18
3934

Perfect score: 1 tccagtaaggagtcggygtc.....aaatctttatcaataa 3934

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapect 60.0

Searched: 441362 segs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2.6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2.6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2.6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2.6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2.6/ptodata/1/ina/PCUS.COMB.seq.*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	0.5	21	US-08-607-269-1	Sequence 1, Appl
C 2	21	0.5	21	PCR-US95-04600-1	Sequence 1, Appl
C 3	20	0.5	20	US-08-607-269-3	Sequence 3, Appl
C 4	20	0.5	20	US-09-226-568-19	Sequence 19, Appl
C 5	20	0.5	20	US-09-226-568-20	Sequence 20, Appl
C 6	20	0.5	20	US-09-226-568-21	Sequence 21, Appl
C 7	20	0.5	20	US-09-226-568-22	Sequence 22, Appl
C 8	20	0.5	20	US-09-226-568-23	Sequence 23, Appl
C 9	20	0.5	20	US-09-226-568-24	Sequence 24, Appl
C 10	20	0.5	20	US-09-226-568-25	Sequence 25, Appl
C 11	20	0.5	20	US-09-226-568-26	Sequence 26, Appl
C 12	20	0.5	20	US-09-226-568-27	Sequence 27, Appl
C 13	20	0.5	20	US-09-226-568-28	Sequence 28, Appl
C 14	20	0.5	20	US-09-226-568-29	Sequence 29, Appl
C 15	20	0.5	20	US-09-226-568-30	Sequence 30, Appl
C 16	20	0.5	20	US-09-226-568-31	Sequence 31, Appl
C 17	20	0.5	20	US-09-226-568-32	Sequence 32, Appl
C 18	20	0.5	20	US-09-226-568-33	Sequence 33, Appl
C 19	20	0.5	20	US-09-226-568-34	Sequence 34, Appl
C 20	20	0.5	20	US-09-226-568-35	Sequence 35, Appl
C 21	20	0.5	20	US-09-226-568-36	Sequence 36, Appl
C 22	20	0.5	20	US-09-226-568-37	Sequence 37, Appl
C 23	20	0.5	20	US-09-226-568-38	Sequence 38, Appl
C 24	20	0.5	20	PCR-US95-04600-3	Sequence 3, Appl
C 25	18	0.5	26	US-08-607-269-17	Sequence 17, Appl
C 26	18	0.5	26	PCR-US95-04600-17	Sequence 17, Appl
C 27	18	0.5	28	PCR-US92-09202-7	Sequence 7, Appl

28	18	0.5	33	1	US-07-954-364-1	Sequence 1, Appl
C 29	18	0.5	38	2	US-08-857-946-106	Sequence 106, App
C 30	18	0.5	38	3	US-08-970-740-106	Sequence 106, App
C 31	18	0.5	41	5	PCR-US92-09202-6	Sequence 6, Appl
C 32	18	0.5	41	5	PCR-US93-07743-5	Sequence 5, Appl
C 33	18	0.5	41	5	PCR-US93-07743-10	Sequence 10, Appl
C 34	17	0.4	24	1	US-08-607-269-16	Sequence 16, Appl
C 35	17	0.4	24	5	PCR-US95-04600-16	Sequence 16, Appl
C 36	17	0.4	28	5	PCR-US92-09202-4	Sequence 4, Appl
C 37	17	0.4	41	5	PCR-US92-09202-3	Sequence 3, Appl
C 38	16	0.4	19	4	US-09-177-953-9	Sequence 9, Appl
C 39	16	0.4	21	2	US-08-863-639A-36	Sequence 36, Appl
C 40	16	0.4	21	2	US-08-863-639A-48	Sequence 48, Appl
C 41	16	0.4	21	2	US-08-863-639A-50	Sequence 50, Appl
C 42	16	0.4	21	2	US-08-863-639A-73	Sequence 73, Appl
C 43	16	0.4	21	2	US-08-863-639A-76	Sequence 76, Appl
C 44	16	0.4	21	2	US-08-863-639A-88	Sequence 88, Appl
C 45	16	0.4	24	1	US-08-160-670A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-607-269-1/c
; Sequence 1, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,269
; FILING DATE:
; CLASSIFICATION: 435.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-607-269-1
Query Match 0.5%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1235 GCAGTGGCAAGAGATTATG 1255
|||||

Db 21 GCAAGTGCAGAGATTATG 1

RESULT 2

PCT-US95-04600-1/c

Sequence 1, Application PC/TUS9504600

GENERAL INFORMATION:

APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION

TITLE OF INVENTION: Interaction of Proteins Involved in

TITLE OF INVENTION: a Cell Death Pathway

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04600

FILING DATE: 12-APR-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Imbra, Richard J.

REGISTRATION NUMBER: 37,643

REFERENCE/DOCKET NUMBER: FP-LJ 1361

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: Linear

PCT-US95-04600-1

Query Match 0.5%; Score 21; DB 5; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1235 GCAAGTGCAGAGATTATG 1255

Db 21 GCAAGTGCAGAGATTATG 1

RESULT 3

US-08-607-269-3/c

Sequence 3, Application US/08607269

Patent No. 5702897

GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Sato, Takaaki

TITLE OF INVENTION: Interaction of Proteins Involved in a

TITLE OF INVENTION: Cell Death Pathway

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/607,269

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/226,876

FILING DATE: 13-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 9882

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: Linear

US-08-607-269-3

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1182 GGACTCCAGCTGTACTTC 1201

Db 20 GGACTCCAGCTGTACTTC 1

RESULT 4

US-09-226-568-19/c

Sequence 19, Application US/09226568

Patent No. 6001992

GENERAL INFORMATION:

APPLICANT: Ackermann, Elizabeth J.

APPLICANT: Bennett, C. Frank

APPLICANT: Dean, Nicholas M.

TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic

FILE REFERENCE: ISPh-0337

CURRENT APPLICATION NUMBER: US/09/226,568

CURRENT FILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentn Ver. 2.0

SEQ ID NO 19

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: antisense

US-09-226-568-19

Query Match 0.5%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GCGACTGCGAATGTTGGC 69

Db 20 GCGACTGCGAATGTTGGC 1

RESULT 5

US-09-226-568-20/c

Sequence 20, Application US/09226568

Patent No. 6001992

GENERAL INFORMATION:

APPLICANT: Ackermann, Elizabeth J.

APPLICANT: Bennett, C. Frank

APPLICANT: Dean, Nicholas M.


```
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-226-568-20
```

```
Query Match          0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 152 CGGAGGCGGACTTTGGCT 171
Db 20 CGGAGGCGGACTTTGGCT 1
```

```
RESULT 6
US-09-226-568-21/c
; Sequence 21, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-226-568-21
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```
Query Match          0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 431 AGGAGCTGACGGGTACGAG 450
Db 20 AGGAGCTGACGGGTACGAG 1
```

```
RESULT 7
US-09-226-568-22/c
; Sequence 22, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
```

```
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-226-568-22
```

```
Query Match          0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 501 CGGGGAATCTGTAATACCA 520
Db 20 CGGGGAATCTGTAATACCA 1
```

```
RESULT 8
US-09-226-568-23/c
; Sequence 23, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-226-568-23
```

```
Query Match          0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 636 GCCCAGGACACAAAGCCAA 655
Db 20 GCCCAGGACACAAAGCCAA 1
```

```
RESULT 9
US-09-226-568-24/c
; Sequence 24, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 24
; LENGTH: 20
```

```
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-226-568-24
```

```
Query Match          0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 842 GGGGCGAGGATGTGACTCTC 861
      |||||||
Db 20 GGGGCGAGGATGTGACTCTC 1
```

```
RESULT 10
US-09-226-568-25/c
Sequence 25, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 25
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-226-568-25
```

```
Query Match          0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1045 AGGAATGCTGCTGCGCTTT 1064
      |||||||
Db 20 AGGAATGCTGCTGCGCTTT 1
```

```
RESULT 11
US-09-226-568-26/c
Sequence 26, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 26
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-226-568-26
```

```
US-09-226-568-26
```

```
Query Match          0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1230 GAAAGCAAGTGGCAAGAG 1249
      |||||||
Db 20 GAAAGCAAGTGGCAAGAG 1
```

```
RESULT 12
US-09-226-568-27/c
Sequence 27, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 27
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-226-568-27
```

```
Query Match          0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1519 AAGATGCCAGTGACCTGTG 1538
      |||||||
Db 20 AAGATGCCAGTGACCTGTG 1
```

```
RESULT 13
US-09-226-568-28/c
Sequence 28, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 28
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-226-568-28
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Query Match          0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1676 GGCTTGTCATGATTCCT 1695
DB 20 GGCTTGTCATGATTCCT 1

Search completed: March 14, 2003, 08:31:50
Job time : 96.137 secs

RESULT 14
US-09-226-568-29/c
; Sequence 29, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-226-568-29

Query Match 0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2091 TGAACCTGGATTGAGAG 2110
DB 20 TGAACCTGGATTGAGAG 1

RESULT 15
US-09-226-568-30/c
; Sequence 30, Application US/09226568
; Patent No. 6001992
; GENERAL INFORMATION:
; APPLICANT: Ackermann, Elizabeth J.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
; FILE REFERENCE: ISPH-0337
; CURRENT APPLICATION NUMBER: US/09/226,568
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-226-568-30

Query Match 0.5%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2231 TGAGTTCCTCCATTGACC 2250
DB 20 TGAGTTCCTCCATTGACC 1

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 07:14:05 ; Search time 247.857 seconds

(without alignments)
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Perfect score: 3934

Sequence: 1 tccagtaagagagtcggggtc.....aaatctttatccaataaa 3934

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 501302 seqs, 350932545 residues

Word size : 0

Total number of hits satisfying chosen parameters: 282380

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/PCVUS_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCVUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	0.4	33	10	US-09-884-814-4
2	16	0.4	17	10	US-09-263-959-900
3	16	0.4	17	10	US-09-263-959-904
4	16	0.4	18	10	US-09-263-959-921
5	16	0.4	21	10	US-09-828-034-11
6	16	0.4	21	10	US-09-828-034-30
7	16	0.4	21	10	US-09-828-034-31
8	16	0.4	22	9	US-10-194-584-12
9	16	0.4	22	10	US-09-814-986-59
10	16	0.4	26	9	US-09-811-824-5
11	16	0.4	30	10	US-09-045-620-3
12	16	0.4	30	10	US-09-728-466-19
13	16	0.4	30	10	US-09-954-697-50
14	16	0.4	33	9	US-09-817-513A-22
15	16	0.4	34	9	US-09-811-824-4
16	16	0.4	43	12	US-10-043-142-4
17	16	0.4	46	9	US-09-966-634-108
18	16	0.4	46	9	US-10-026-914-8
19	16	0.4	46	9	US-10-026-914-10

C 20	16	0.4	46	9	US-10-026-914-14	Sequence 14, Appl
C 21	16	0.4	46	9	US-10-026-914-16	Sequence 16, Appl
C 22	16	0.4	47	9	US-10-026-914-4	Sequence 4, Appl
C 23	16	0.4	48	10	US-09-801-042-8	Sequence 8, Appl
C 24	16	0.4	48	12	US-10-082-018-6	Sequence 6, Appl
C 25	16	0.4	50	10	US-09-935-727-26	Sequence 26, Appl
C 26	15	0.4	18	10	US-09-969-373-2606	Sequence 2606, Ap
C 27	15	0.4	27	10	US-09-873-676-74	Sequence 74, Appl
C 28	15	0.4	30	9	US-09-976-736-27	Sequence 27, Appl
C 29	15	0.4	31	9	US-09-912-263-155	Sequence 155, Appl
C 30	15	0.4	44	10	US-09-007-093-16	Sequence 16, Appl
C 31	15	0.4	46	9	US-10-137-316-5	Sequence 5, Appl
C 32	15	0.4	46	9	US-10-137-316-7	Sequence 7, Appl
C 33	14	0.4	18	9	US-09-961-077-1149	Sequence 1149, Ap
C 34	14	0.4	19	10	US-09-736-863-16	Sequence 16, Appl
C 35	14	0.4	20	9	US-09-863-806-85	Sequence 85, Appl
C 36	14	0.4	20	10	US-09-800-629A-27	Sequence 27, Appl
C 37	14	0.4	21	10	US-09-828-034-9	Sequence 9, Appl
C 38	14	0.4	21	10	US-09-828-034-28	Sequence 28, Appl
C 39	14	0.4	22	10	US-09-263-959-1093	Sequence 1093, Ap
C 40	14	0.4	23	10	US-09-735-995-17	Sequence 17, Appl
C 41	14	0.4	23	10	US-09-735-995-73	Sequence 73, Appl
C 42	14	0.4	24	9	US-09-911-1768-27	Sequence 27, Appl
C 43	14	0.4	24	9	US-09-804-177A-30	Sequence 30, Appl
C 44	14	0.4	24	9	US-10-180-762-27	Sequence 27, Appl
C 45	14	0.4	25	9	US-09-755-088-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-884-814-4
; Sequence 4, Application US/09884814
; Patent No. US20020127600A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 018/81-001100S
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 09/884, 814
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:U8R primer
US-09-884-814-4
Query Match 0.4%; score 17; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 453 GGAGCCTCTCGGAGC 469
DB 17 GGAGCCTCTCGGAGC 33
RESULT 2
US-09-263-959-900
; Sequence 900, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Roven, Lee
; APPLICANT: Koop, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 900:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-900

Query Match 0.4%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCACGACGACGACCA 1163
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Db 1 ACCACGACGACGACCA 16

RESULT 3
US-09-263-959-904
Sequence 904, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 904:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-904

Query Match 0.4%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCACGACGACGACCA 1163
|||||

Db 2 ACCACGACGACGACCA 17

RESULT 4
US-09-263-959-921
Sequence 921, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 921:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-921

Query Match 0.4%; Score 16; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCACGACGACGACCA 1163
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Db 1 ACCACGACGACGACCA 16

RESULT 5
US-09-828-034-11
Sequence 11, Application US/09828034
Patent No. US20020064771A1

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; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-11
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Query Match          0.4%; Score 16; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1148 ACCACCACACACCA 1163
      |||
Db 1 ACCACCACACACCA 16
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RESULT 5
US-09-828-034-30
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; Sequence 30, Application US/09828034
; Patent No. US2002006477A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-30
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Query Match          0.4%; Score 16; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1148 ACCACCACACACCA 1163
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Db 3 ACCACCACACACCA 18
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RESULT 7
US-09-828-034-31
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; Sequence 31, Application US/09828034
; Patent No. US2002006477A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
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; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-31
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Query Match          0.4%; Score 16; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1148 ACCACCACACACCA 1163
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Db 2 ACCACCACACACCA 17
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RESULT 8
US-10-194-594-12/C
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; Sequence 12, Application US/10194594
; Publication No. US2003004386A1
; GENERAL INFORMATION:
; APPLICANT: Barber, Glen
; TITLE OF INVENTION: RECOMBINANT VSV FOR THE TREATMENT OF
; TITLE OF INVENTION: TUMOR CELLS
; FILE REFERENCE: 529372000200
; CURRENT APPLICATION NUMBER: US/10/194,594
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US 60/304,125
; PRIOR FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Vesicular stomatitis virus
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: (2)...(12)
; OTHER INFORMATION: Polyadenylation/transcription stop signal of the
; OTHER INFORMATION: glycoprotein (G) gene
; NAME/KEY: misc_feature
; LOCATION: (15)...(19)
; OTHER INFORMATION: Start sequence of the RNA polymerase L protein
US-10-194-594-12
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Query Match          0.4%; Score 16; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1866 TTAGTTTTTTCATAC 1881
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Db 16 TTAGTTTTTTCATAC 1
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RESULT 9
US-09-814-986-59
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; Sequence 59, Application US/09814986
; Patent No. US20020068286A1
; GENERAL INFORMATION:
; APPLICANT: Kieyu, Patrick W.
; APPLICANT: Kieyu, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/814,986
FILING DATE: 22-Mar-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/936,707
FILING DATE: 24-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PERNIE
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-814-986-59
Query Match 0.4%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1148 ACCACGACGACGACCA 1163
DB 2 ACCACGACGACGACCA 17
RESULT 10
US-09-811-824-5/c
Sequence 5, Application US/09811824
Publication No. US20020182632A1
GENERAL INFORMATION:
APPLICANT: Anderson, George P.
APPLICANT: Matloussi, Bedi
APPLICANT: Mauro, J. Matthew
APPLICANT: Bawendi, Moungi G.
APPLICANT: Sundar, Vikram C.
TITLE OF INVENTION: INORGANIC PARTICLE CONJUGATES
FILE REFERENCE: 01997-282001
CURRENT APPLICATION NUMBER: US/09/811,824
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,766
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
TYPE: DNA
LENGTH: 26
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated primer
US-09-811-824-5
Query Match 0.4%; Score 16; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCACGACGACGACCA 1163
DB 21 ACCACGACGACGACCA 6
RESULT 11
US-09-045-620-3/c
Sequence 3, Application US/09045620
Patent No. US20010006793A1
GENERAL INFORMATION:
APPLICANT: BJORNSTI, Mary-Ann
APPLICANT: HAL, David
APPLICANT: KANG, Jason
TITLE OF INVENTION: MODULATORS OF EUKARYOTIC CASPASES
FILE REFERENCE: 209855.0027/2705
CURRENT APPLICATION NUMBER: US/09/045,620
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Caspase CDNA
US-09-045-620-3
Query Match 0.4%; Score 16; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1148 ACCACGACGACGACCA 1163
DB 29 ACCACGACGACGACCA 14
RESULT 12
US-09-728-466-19/c
Sequence 19, Application US/09728466
Patent No. US20010029022A1
GENERAL INFORMATION:
APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/728,466
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-728-466-19
Query Match 0.4%; Score 16; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1148 ACCACGACGACGACCA 1163
DB 28 ACCACGACGACGACCA 13
RESULT 13
US-09-954-697-50/c
Sequence 50, Application US/09954697


```
Patent No. US2002010631A1
GENERAL INFORMATION:
  APPLICANT: Alnemt, Emd S.
  TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USBS
  TITLE OF INVENTION: THEREOF
  FILE REFERENCE: 480140.431D2
  CURRENT APPLICATION NUMBER: US/09/954,697
  CURRENT FILING DATE: 2001-09-14
  NUMBER OF SEQ ID NOS: 116
  SOFTWARE: FastSeq for Windows Version 3.0
  SEQ ID NO: 50
  LENGTH: 30
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: PCR primer for small subunit of caspase-6
US-09-954-697-50

Query Match
  0.4%; Score 16; DB 10; Length 30;
  Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCACCCACCCACCA 1163
DB 28 ACCACCCACCCACCA 13

RESULT 14
US-09-817-513A-22
  Sequence 22, Application US/09817513A
  Publication No. US20030044958A1
  GENERAL INFORMATION:
  APPLICANT: Staunton, Donald E.
  TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
  Binding/Signalling
  NUMBER OF SEQUENCES: 30
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  STREET: 233 South Wacker, 6300 Sears Tower
  CITY: Chicago
  STATE: Illinois
  COUNTRY: USA
  ZIP: 60606
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/817,513A
  FILING DATE: 28-Jun-2001
  CLASSIFICATION: <Unknown>
  ATTORNEY/AGENT INFORMATION:
  NAME: Young J. Suh
  REGISTRATION NUMBER: P-41,337
  REFERENCE/DOCKET NUMBER: 27866/33886
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 312-474-6300
  TELEFAX: 312-474-0448
  INFORMATION FOR SEQ ID NO: 22:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 33 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: other nucleic acid
  DESCRIPTION: /desc = "primer"
  SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-817-513A-22

Query Match
  0.4%; Score 16; DB 9; Length 33;
  Best Local Similarity 100.0%; Pred. No. 6.9e+02;
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```
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1361 AGCTATGGAGGAGGAC 1376
DB 9 AGCTATGGAGGAGGAC 24

RESULT 15
US-09-811-824-4
  Sequence 4, Application US/09811824
  Publication No. US20020182632A1
  GENERAL INFORMATION:
  APPLICANT: Anderson, George P.
  APPLICANT: Matlousi, Hedi
  APPLICANT: Mauro, J. Mathew
  APPLICANT: Bavendi, Mounqi G.
  APPLICANT: Sundar, Vikram C.
  TITLE OF INVENTION: INORGANIC PARTICLE CONJUGATES
  FILE REFERENCE: 01997-282001
  CURRENT APPLICATION NUMBER: US/09/811,824
  PRIOR FILING DATE: 2001-03-20
  PRIOR APPLICATION NUMBER: US 60/190,766
  NUMBER OF SEQ ID NOS: 7
  SOFTWARE: FastSeq for Windows Version 4.0
  SEQ ID NO: 4
  LENGTH: 34
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Synthetically generated primer
US-09-811-824-4

Query Match
  0.4%; Score 16; DB 9; Length 34;
  Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCACCCACCCACCA 1163
DB 10 ACCACCCACCCACCA 25
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Search completed: March 14, 2003, 10:59:24
Job time : 249.857 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 04:35:16 ; Search time 5795.01 Seconds
(without alignments)
17068.215 Million cell updates/sec

Title: US-09-869-894-18

Perfect score: 3934
Sequence: 1 tccaagaaggagtcggggtc.....aaatctttatccaataaa 3934

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum Db seq length: 0
Maximum Db seq length: 50

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	46	1.2	46	US-08-472-801-2244	Sequence 2244, Ap
C 2	46	1.2	46	US-08-668-235-2244	Sequence 2244, Ap
C 3	42	1.1	42	US-08-472-801-2235	Sequence 2235, Ap
C 4	42	1.1	42	US-08-668-235-2235	Sequence 2235, Ap
C 5	40	1.0	40	US-08-472-801-2249	Sequence 2249, Ap
C 6	40	1.0	40	US-08-668-235-2249	Sequence 2249, Ap
C 7	35	0.9	35	US-08-472-801-2258	Sequence 2258, Ap
C 8	35	0.9	35	US-08-668-235-2258	Sequence 2258, Ap
C 9	35	0.9	35	US-08-472-801-2262	Sequence 2262, Ap
C 10	35	0.9	35	US-08-668-235-2262	Sequence 2262, Ap
C 11	34	0.9	34	US-08-472-801-2233	Sequence 2233, Ap
C 12	34	0.9	34	US-08-668-235-2233	Sequence 2233, Ap
C 13	34	0.9	34	US-08-472-801-2249	Sequence 2249, Ap
C 14	34	0.9	34	US-08-668-235-2249	Sequence 2249, Ap
C 15	34	0.9	34	US-08-472-801-2258	Sequence 2258, Ap
C 16	34	0.9	34	US-08-668-235-2258	Sequence 2258, Ap
C 17	32	0.8	32	US-08-472-801-2252	Sequence 2252, Ap
C 18	32	0.8	32	US-08-668-235-2252	Sequence 2252, Ap
C 19	31	0.8	31	US-08-472-801-2231	Sequence 2231, Ap
C 20	31	0.8	31	US-08-668-235-2231	Sequence 2231, Ap
C 21	31	0.8	31	US-08-472-801-2247	Sequence 2247, Ap
C 21	31	0.8	31	US-08-668-235-2247	Sequence 2247, Ap

```

c 22 31 0.8 31 10 US-08-668-235-2231 Sequence 2231, Ap
c 23 31 0.8 31 10 US-08-668-235-2247 Sequence 2247, Ap
c 24 31 0.8 31 10 US-08-668-235-2255 Sequence 2255, Ap
c 25 30 0.8 30 1 PCR-US00-00969-19 Sequence 19, Appl
c 26 30 0.8 30 18 US-09-483-184-19 Sequence 19, Appl
c 27 24 0.6 24 8 US-08-472-801-2234 Sequence 2234, Ap
c 28 24 0.6 24 8 US-08-472-801-2254 Sequence 2254, Ap
c 29 24 0.6 24 10 US-08-668-235-2234 Sequence 2234, Ap
c 30 24 0.6 24 10 US-08-668-235-2254 Sequence 2254, Ap
c 31 23 0.6 23 8 US-08-472-801-2236 Sequence 2236, Ap
c 32 23 0.6 23 8 US-08-472-801-2240 Sequence 2240, Ap
c 33 23 0.6 23 8 US-08-472-801-2248 Sequence 2248, Ap
c 34 23 0.6 23 8 US-08-472-801-2250 Sequence 2250, Ap
c 35 23 0.6 23 8 US-08-472-801-2251 Sequence 2251, Ap
c 36 23 0.6 23 8 US-08-472-801-2253 Sequence 2253, Ap
c 37 23 0.6 23 8 US-08-472-801-2255 Sequence 2255, Ap
c 38 23 0.6 23 10 US-08-668-235-2236 Sequence 2236, Ap
c 39 23 0.6 23 10 US-08-668-235-2240 Sequence 2240, Ap
c 40 23 0.6 23 10 US-08-668-235-2248 Sequence 2248, Ap
c 41 23 0.6 23 10 US-08-668-235-2250 Sequence 2250, Ap
c 42 23 0.6 23 10 US-08-668-235-2251 Sequence 2251, Ap
c 43 23 0.6 23 10 US-08-668-235-2253 Sequence 2253, Ap
c 44 23 0.6 23 10 US-08-668-235-2259 Sequence 2259, Ap
c 45 23 0.6 38 1 PCR-US02-15045-5 Sequence 5, Appl

```

ALIGNMENTS

```

RESULT 1
US-08-472-801-2244/c
; Sequence 2244, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hessed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; FILE REFERENCE: Hessed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2244
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2244

```

```

Query Match 1.1%; Score 46; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 8.6e-11;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 534 GTGACTACCTCGACGCCGCCGCGGAGAGAGAGAGAGAGAG 579
Db 46 GTGACTACCTCGACGCCGCCGCGGAGAGAGAGAGAGAGAGAG 1

```

```

RESULT 2
US-08-668-235-2244/c
; Sequence 2244, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; FILE REFERENCE: Hessed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95

```

```

; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2244
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2244

```

```

Query Match 1.2%; Score 46; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 8.6e-11;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 534 GTGACTACCTCGACGCCGCCGCGGAGAGAGAGAGAGAGAG 579
Db 46 GTGACTACCTCGACGCCGCCGCGGAGAGAGAGAGAGAGAGAG 1

```

```

RESULT 3
US-08-472-801-2235/c
; Sequence 2235, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hessed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; FILE REFERENCE: Hessed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2235
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2235

```

```

Query Match 1.1%; Score 42; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 192 CGGCGAGAGATGAGGGGAGGGGCGCGCGCGGTGATTGG 233
Db 42 CGGCGAGAGATGAGGGGAGGGGCGCGCGCGGTGATTGG 1

```

```

RESULT 4
US-08-668-235-2235/c
; Sequence 2235, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; FILE REFERENCE: Hessed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2235
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2235

```

```

Query Match 1.1%; Score 42; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Oy 192 CCGCGAGATAGAGGGGAGGCGCGCGGATTTG 233
      |||||||
Db 42 CCGCGAGATAGAGGGGAGGAGGCGCGCGGATTTG 1

RESULT 5
US-08-472-801-2249/c
; Sequence 2249, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hessed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; FILE REFERENCE: Hessed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2249
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2249

Query Match 1.0%; Score 40; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3215 GGAAGAACTGCGCTGCTGCATCTCAGAGCCATAGGT 3254
      |||||||
Db 40 GGAAGAACTGCGCTGCTGCATCTCAGAGCCATAGGT 1

RESULT 6
US-08-668-235-2249/c
; Sequence 2249, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; FILE REFERENCE: Hessed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2249
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2249

Query Match 1.0%; Score 40; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3215 GGAAGAACTGCGCTGCTGCATCTCAGAGCCATAGGT 3254
      |||||||
Db 40 GGAAGAACTGCGCTGCTGCATCTCAGAGCCATAGGT 1

RESULT 7
US-08-472-801-2258/c
; Sequence 2258, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hessed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
```

```
; TITLE OF INVENTION: Reprogramming
; FILE REFERENCE: Hessed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2258
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2258

Query Match 0.9%; Score 35; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 403 GCCGCTGACGCCATCATGTGCCCGAAGAGAGCT 437
      |||||||
Db 35 GCCGCTGACGCCATCATGTGCCCGAAGAGAGCT 1

RESULT 8
US-08-472-801-2262/c
; Sequence 2262, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hessed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; FILE REFERENCE: Hessed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2262
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2262

Query Match 0.9%; Score 35; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 628 GCCACCGGCGCAAGACACCAAGCCATGGGCG 662
      |||||||
Db 35 GCCACCGGCGCAAGACACCAAGCCATGGGCG 1

RESULT 9
US-08-668-235-2258/c
; Sequence 2258, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; FILE REFERENCE: Hessed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2258
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2258
```

```

Query Match      0.9%; Score 35; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 GCCGCTGACGCATCATGTCCCGGAGAGAGAGCT 437
    |||||||
DB 35 GCCGCTGACGCATCATGTCCCGGAGAGAGAGCT 1

RESULT 10
US-08-668-235-2262/c
; Sequence 2262, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; FILE REFERENCE: Hseshed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; EARLIER FILING DATE: 1996-06-17/748,997
; EARLIER APPLICATION NUMBER: 08/23/91
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2262
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2262

Query Match      0.9%; Score 35; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 628 GCCACCGGCGCCAGACACAAAGCCATGGGCGAG 662
    |||||||
DB 35 GCCACCGGCGCCAGACACAAAGCCATGGGCGAG 1

RESULT 11
US-08-472-801-2233/c
; Sequence 2233, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hseshed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; FILE REFERENCE: Hseshed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2233
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2233

Query Match      0.9%; Score 34; DB 8; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 CCCGGAGGCGACTTTGGCTACGAGAGAGAG 183
    |||||||
DB 34 CCCGGAGGCGACTTTGGCTACGAGAGAGAG 1

RESULT 12
US-08-472-801-2239/c
; Sequence 2239, Application US/08472801

```

```

; GENERAL INFORMATION:
; APPLICANT: Hseshed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; FILE REFERENCE: Hseshed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2239
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2239

Query Match      0.9%; Score 34; DB 8; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 CCACCTGACGCCGAGACTCCGAGAGGTGCGCGC 293
    |||||||
DB 34 CCACCTGACGCCGAGACTCCGAGAGGTGCGCGC 1

RESULT 13
US-08-472-801-2242/c
; Sequence 2242, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hseshed 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; FILE REFERENCE: Hseshed 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2242
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-2242

Query Match      0.9%; Score 34; DB 8; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 CGCTGCTGAGAGTGTGCGGAGATCTGTATATA 518
    |||||||
DB 34 CGCTGCTGAGAGTGTGCGGAGATCTGTATATA 1

RESULT 14
US-08-668-235-2233/c
; Sequence 2233, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; FILE REFERENCE: Hseshed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; CURRENT FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2233
; LENGTH: 34

```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2239

Query Match                      0.9%; Score 34; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 CCGGAGGAGCGACTTTTGGCTACGAGAGAG 183
      ||||||||||||||||||||||||||||
Db 34 CCGGAGGAGCGACTTTTGGCTACGAGAGAG 1

RESULT 15
US-08-668-235-2239/c
; Sequence 2239, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; FILE REFERENCE: Hersed-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; EARLIER FILING DATE: 1996-06-17
; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2239
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-2239

Query Match                      0.9%; Score 34; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 CCACCTCACGCCAGACTCCGAGAGGTCGCCG 293
      ||||||||||||||||||||||||||||
Db 34 CCACCTCACGCCAGACTCCGAGAGGTCGCCG 1

Search completed: March 14, 2003, 10:28:01
Job time : 5797.01 secs
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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 04:47:29 ; Search time 1076.55 Seconds

(without alignments)
8302.956 Million cell updates/sec

Title: US-09-869-894-18
Perfect score: 3934
Sequence: 1 tccaggaagagagtcggggc.....aaatttttatacaataaa 3934

Scoring table: ORIGO_NMC
Gapop 60.0 , Gapect 60.0

Searched: 466902 seqs, 1136064160 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7027196

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	0.6	25	US-10-236-392-256	Sequence 256, App
2	24	0.6	24	US-10-293-338-8053	Sequence 8053, App
3	24	0.6	24	US-10-310-188-79749	Sequence 79749, A
4	23	0.6	25	US-60-427-836-454577	Sequence 454577, A
5	22	0.6	22	US-10-310-188-2008	Sequence 2068, App
6	21	0.5	21	US-10-310-188-7862	Sequence 7862, App
7	21	0.5	21	US-10-310-188-73447	Sequence 73447, A
8	20	0.5	25	US-10-355-577-900097	Sequence 900097, A
9	20	0.5	20	US-10-293-338-3254	Sequence 3254, App
10	20	0.5	20	US-10-310-188-81944	Sequence 81944, A
11	20	0.5	20	US-10-169-983-57	Sequence 57, App
12	20	0.5	20	US-60-427-808-23817	Sequence 23817, A
13	20	0.5	25	US-10-293-338-1275	Sequence 1275, App
14	19	0.5	19	US-10-310-188-57069	Sequence 57069, A
15	19	0.5	19	US-10-310-188-68525	Sequence 68525, A
16	19	0.5	19	US-10-310-188-56931	Sequence 56931, A
17	19	0.5	18	US-10-303-778-1607	Sequence 1607, App
18	18	0.5	18	US-10-303-778-8650	Sequence 8650, App
19	18	0.5	18	US-10-310-188-744	Sequence 744, App
20	18	0.5	21	US-10-310-188-79750	Sequence 79750, A
21	18	0.5	25	US-60-427-808-541112	Sequence 541112, A
22	18	0.5	25	US-60-427-836-102497	Sequence 102497, A
23	18	0.5	25	US-60-427-836-102497	Sequence 102497, A
24	18	0.5	25	US-60-427-836-237621	Sequence 237621, A

c 25	18	0.5	25	9	US-60-427-836-571386	Sequence 571386, App
c 26	18	0.5	41	9	US-60-449-155-609	Sequence 16089, App
c 27	17	0.4	17	8	US-10-303-778-16089	Sequence 31362, A
c 28	17	0.4	17	8	US-10-310-188-31362	Sequence 255, App
c 29	17	0.4	17	8	US-10-236-392-255	Sequence 79759, A
c 30	17	0.4	18	8	US-10-310-188-79759	Sequence 48654, A
c 31	17	0.4	20	8	US-10-310-188-48654	Sequence 29017, A
c 32	17	0.4	21	8	US-10-310-188-29017	Sequence 62082, A
c 33	17	0.4	21	8	US-10-310-188-62082	Sequence 7439, App
c 34	17	0.4	25	8	US-10-355-577-7439	Sequence 106353, App
c 35	17	0.4	25	8	US-10-355-577-106353	Sequence 476248, App
c 36	17	0.4	25	8	US-10-355-577-476248	Sequence 870929, App
c 37	17	0.4	25	9	US-60-427-808-136571	Sequence 136571, App
c 38	17	0.4	25	9	US-60-427-808-179014	Sequence 179014, App
c 39	17	0.4	25	9	US-60-427-808-409599	Sequence 409599, App
c 40	17	0.4	25	9	US-60-427-808-65488	Sequence 65488, App
c 41	17	0.4	25	9	US-60-427-836-321372	Sequence 321372, App
c 42	17	0.4	32	7	US-10-287-787-13609	Sequence 13609, App
c 43	17	0.4	42	8	US-10-050-902-297	Sequence 297, App
c 44	17	0.4	42	8	US-10-050-902-298	Sequence 298, App
c 45	17	0.4	42	8	US-10-050-902-298	Sequence 298, App

ALIGNMENTS

RESULT 1
US-10-236-392-256/c
; Sequence 256, Application US/10236392
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Laroche, William J
; APPLICANT: Li, Li
; APPLICANT: Macdonald, John R
; APPLICANT: Malyskari, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patlurajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OR INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303

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; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 256
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: probe
US-10-236-392-256

```

```

Query Match      0.6%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 678 CAGGAAGCGCTGGAGACCTTACGA 702
|||||
DB 25 CAGGAAGCGCTGGAGACCTTACGA 1

```

```

RESULT 2
US-10-293-338-8053/c
; Sequence 8053, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293,338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8053
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-8053

```

```

Query Match      0.6%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1330 AGTTTCACGACAAACAACCTTG 1353
|||||
DB 24 AGTTTCACGACAAACAACCTTG 1

```

```

RESULT 3
US-10-310-188-79749/c
; Sequence 79749, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79749
; LENGTH: 24
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
US-10-310-188-79749

```

```

Query Match      0.6%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1146 CAACGACGACGACGACCAAAACCA 1169
|||||
DB 24 CAACGACGACGACGACCAAAACCA 1

```

```

RESULT 4
US-60-427-836-454577
; Sequence 454577, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 454577
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-454577

```

```

Query Match      0.6%; Score 23; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 748 GGCATGCTCGGAACCTGACAT 770
|||||
DB 2 GGCATGCTCGGAACCTGACAT 24

```

```

RESULT 5
US-10-310-188-2068/c
; Sequence 2068, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2068
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-2068

```

```

Query Match      0.6%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2430 GCAGGCTAGCTAACATGTG 2451
|||||
DB 22 GCAGGCTAGCTAACATGTG 1

```

```

RESULT 6
US-10-310-188-7862/c
; Sequence 7862, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487

```

```

; CURRENT APPLICATION NUMBER: US/10/310.188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7862
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-7862

Query Match          0.5%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

QY 3541 ACACCCCAAGTGTGGGAA 3561
DB 21 ACACCCCAAGTGTGGGAA 1

RESULT 7
US-10-310-188-73447/C
; Sequence 73447, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: Rosettagenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310.188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73447
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-73447

Query Match          0.5%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

QY 1211 CACCTAGCACTAGCCAA 1231
DB 21 CACCTAGCACTAGCCAA 1

RESULT 8
US-10-355-577-90097
; Sequence 90097, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-VL33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355.577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 300097
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-355-577-90097

Query Match          0.5%; Score 21; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3578 GGGTTATAGGGAGAGAGAG 3598
DB 5 GGGTTATAGGGAGAGAGAG 25

RESULT 9
US-10-293-338-3254/C
; Sequence 3254, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: Rosettagenomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293.338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3254
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-3254

Query Match          0.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1308 CTGCTGAAGAGCAAGT 1327
DB 20 CTGCTGAAGAGCAAGT 1

RESULT 10
US-10-310-188-81944/C
; Sequence 81944, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: Rosettagenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310.188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81944
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-81944

Query Match          0.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2636 TGAATTGCTGATGCTCTG 2655
DB 20 TGAATTGCTGATGCTCTG 1

RESULT 11
US-10-169-983-57
; Sequence 57, Application US/10169983
; GENERAL INFORMATION:
; APPLICANT: Takara Shuzo Co., Ltd.
; TITLE OF INVENTION: Therapeutic agents
; FILE REFERENCE: 01-011-PCT
; CURRENT APPLICATION NUMBER: US/10/169.983
; CURRENT FILING DATE: 2002-07-14
; PRIOR APPLICATION NUMBER: JP 2000-4989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: JP 2000-303711
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed primer based on nucleotide sequence of
```

OTHER INFORMATION: human myeloid leukemia cell differentiation protein-1 mRNA.
US-10-169-983-57

Query Match 0.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 749 GCATGCTCGGAACCTGAC 768
DB 1 GCATGCTCGGAACCTGAC 20

RESULT 12
US-10-169-983-58/c

Sequence 38, Application US/10169983
GENERAL INFORMATION:
APPLICANT: Takara Shuzo Co., Ltd.
TITLE OF INVENTION: Therapeutic agents
FILE REFERENCE: 01-011-PCT
CURRENT APPLICATION NUMBER: US/10/169,983
CURRENT FILING DATE: 2002-07-14
PRIOR APPLICATION NUMBER: JP 2000-4989
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: JP 2000-303711
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 58
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Designed primer based on nucleotide sequence of
US-10-169-983-58
OTHER INFORMATION: human myeloid leukemia cell differentiation protein-1 mRNA.

Query Match 0.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1182 GGACGTCAGGCTGTAACCTC 1201
DB 20 GGACGTCAGGCTGTAACCTC 1

RESULT 13
US-60-427-808-23817
Sequence 23817, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 23817
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-60-427-808-23817

Query Match 0.5%; Score 20; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AATGTCGCTGCTTTGCT 1067
DB 2 AATGTCGCTGCTTTGCT 21

RESULT 14
US-10-293-338-1275/c
Sequence 1275, Application US/10293338

GENERAL INFORMATION:
APPLICANT: RosettaGenomics Ltd
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES A
FILE REFERENCE: THEREOF
CURRENT APPLICATION NUMBER: 45282
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1275
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-10-293-338-1275

Query Match 0.5%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1772 ATCTTAAGACAGCTGTA 1790
DB 19 ATCTTAAGACAGCTGTA 1

RESULT 15
US-10-310-188-57069/c
Sequence 57069, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57069
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-57069

Query Match 0.5%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1133 GTTGACTTTTAACCAACCA 1151
DB 19 GTTGACTTTTAACCAACCA 1

Search completed: March 14, 2003, 10:49:54
Job time : 1078.55 secs

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 04:32:49 ; Search time 3692.82 Seconds
(without alignments)
17253.226 Million cell updates/sec

Title: US-09-869-894-18

Sequence: 1 tccagtaaggagtcgggggtc.....aaatttttaataa 3934

Scoring table: OLIGO_NTC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database :

EST.*
1: em_estdb.*
2: em_esthm.*
3: em_estln.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pin.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	0.8	31	9	AA463890
2	23	0.6	26	17	AZ365602
3	21	0.5	34	17	AZ343185
4	19	0.5	49	9	A1569150
5	18	0.5	35	17	AZ304663
6	18	0.5	44	17	AZ453451

C 7	17	0.4	28	17	AZ403083
C 8	17	0.4	40	14	H28644
C 9	17	0.4	13	17	AZ637149
C 10	16	0.4	19	17	AZ315293
C 11	16	0.4	20	17	AZ622226
C 12	16	0.4	23	17	AZ784648
C 13	16	0.4	23	17	AZ860972
C 14	16	0.4	24	17	AZ449706
C 15	16	0.4	26	17	AZ405428
C 16	16	0.4	28	17	AZ512393
C 17	16	0.4	28	17	AZ947343
C 18	16	0.4	30	17	AZ821583
C 19	16	0.4	33	17	AZ401045
C 20	16	0.4	33	17	AZ829628
C 21	16	0.4	36	17	AZ346286
C 22	16	0.4	37	17	AZ350D5P
C 23	16	0.4	41	17	AZ662472
C 24	16	0.4	42	17	AZ632020
C 25	16	0.4	45	17	AZ602225
C 26	16	0.4	46	17	AZ939393
C 27	16	0.4	48	17	AZ489134
C 28	16	0.4	50	17	AZ657819
C 29	16	0.4	50	17	AZ964472
C 30	15	0.4	25	13	BG927349
C 31	15	0.4	26	17	AZ479681
C 32	15	0.4	32	17	AZ792853
C 33	15	0.4	33	10	AM698829
C 34	15	0.4	34	17	AZ936680
C 35	15	0.4	35	17	AZ999984
C 36	15	0.4	37	17	AZ392980
C 37	15	0.4	37	17	BH863503
C 38	15	0.4	40	17	AZ788014
C 39	15	0.4	41	17	AZ390426
C 40	15	0.4	43	9	AA209184
C 41	15	0.4	48	17	AZ300919
C 42	15	0.4	50	9	AUI02484
C 43	15	0.4	50	9	AUI03585
C 44	15	0.4	50	9	AUI06893
C 45	15	0.4	50	9	AUI06894

ALIGNMENTS

RESULT 1
LOCUS AA463890
DEFINITION aa08d03.s1 Soares_NhMpu_S1 Homo sapiens cDNA clone IMAGE:812645 3', similar to SW:MCIL_HUMAN_007820 INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL1., mRNA sequence.

ACCESSION AA463890
VERSION AA463890
KEYWORDS AA463890.1 GI:2188774
EST.
SOURCE human
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 31)
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Stepec, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Willson, R.

TITLE Unpublished EST project 1997
JOURNAL Contact: Wilson RK

COMMENT

Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LIND, contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand

Seq primer: -41ml3 fwd. Er from Amerisham
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. .31
/organism="Homo sapiens"
/db_xref="GDB:604355"
/db_xref="taxon:9606"
/clone="IMAGE:812645"
/clone_lib="Soares_NbHNPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10b"
/note="Organ: mixed (see below): Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site1: Not 1; Site2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2nbm, pregnant uterus NbHNPu, and fetal heart NbHNPu) were mixed, and ss cicles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT
ORIGIN

6 a 9 c 13 g 3 t

Query Match 0.8%; Score 30; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 375 GGCGCGCTTGAGGATGAGAGCCCCGGC 404

DB 1 GGCGCGCTTGAGGATGAGAGCCCCGGC 30

RESULT 2

AZ365602/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

26 bp DNA linear GSS 02-OCT-2000
1M012017 Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCGM0112017 F, DNA sequence.
AZ365602
AZ365602.1 GI:10479302
GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: 0 column: 17
Seq primer: CCGTGTAAAGACGAGCGCCACT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. .26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

FEATURES

source

/clone="UGCGM0112017"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: pMD42nv; purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (q1473214|9b|A129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

0 a 1 c 14 g 11 t

Query Match 0.6%; Score 23; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.9;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1148 ACCACACACACACACAAACAG 1170

DB 23 ACCACACACACACACAAACAG 1

RESULT 3

AZ343185/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

34 bp DNA linear GSS 29-SEP-2000
1M0076C22R Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCGM0076C22 R, DNA sequence.
AZ343185
AZ343185.1 GI:10421362
GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 22
Seq primer: CACACGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers
1. .34
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

FEATURES

source

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/clone="UUGC1M0076C22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (q114732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.

BASE COUNT      0 a      0 c      21 g      13 t
ORIGIN
Query Match      0.5%; Score 21; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCACGACGACGACCAAAAC 1168
|||||
Db 23 ACCACGACGACGACCAAAAC 3

RESULT 4
LOCUS A1569150 49 bp mRNA linear EST 29-MAR-1999
DEFINITION t83a03.x1 NCI-CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224876.3',
A1569150
VERSION A1569150.1 GI:4532524
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bcrfemail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www.bio.lnl.gov/bdnp/image/image.html
Seq primer: -400p from gibco.
FEATURES
source
Location/Qualifiers
1..49
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/db_xref="taxon:9606"
/clone="IMAGE:2224876"
/clone_lib="NCI-CGAP_Pan1"
/tissue_type="adrenocarcinoma"
/lab_host="DH10B"
/notes="Organ: pancreas; Vector: PCMV-SPORT6; Site:1; Salt;
Site:2; Nct1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
BASE COUNT      18 a      7 c      2 g      22 t

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ORIGIN
Query Match      0.5%; Score 19; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1797 TTTGTAATAATTGTATATA 1815
|||||
Db 41 TTTGTAATAATTGTATATA 23

RESULT 5
LOCUS A2304663 35 bp DNA linear GSS 29-SEP-2000
DEFINITION M0004016R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0004016 R, DNA sequence.
ACCESSION A2304663
VERSION A2304663.1 GI:10340903
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 35)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 Row: 0 Column: 16
Seq primer: CACACAGGAACACGATGACG
Class: plasmid ends
High quality sequence stop: 35.
FEATURES
source
Location/Qualifiers
1..35
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0004016"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (q114732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      2 a      2 c      18 g      13 t

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ORIGIN

Query Match 0.5%; Score 18; DB 17; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1148 ACCACGACGACGACGACAA 1165
 ||||||||||||||||
 Db 26 ACCACGACGACGACGACAA 9

RESULT 6

AZ453451/c 44 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0254P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0254P10 R, DNA sequence.

ACCESSION AZ453451
 VERSION AZ453451.1 GI:10611092
 KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 44)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY of Utah Genome Center
 UNIVERSITY of Utah
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0254 row: P column: 10
 SEQ PRIMER: CACACGAGAACACGCTATGACC
 CLASS: plasmid ends
 HIGH QUALITY sequence stop: 44.
 Location/Qualifiers

JOURNAL COMMENT

1. 44
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0254P10"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g11473211419b/AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

SOURCE

BASE COUNT

2 a 2 c 15 g 25 t

ORIGIN

Query Match 0.5%; Score 18; DB 17; Length 44;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1147 AACACGACGACGACGACAA 1164
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 Db 38 AACACGACGACGACGACAA 21

RESULT 7

AZ403083 28 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0170P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0170P09 R, DNA sequence.

ACCESSION AZ403083
 VERSION AZ403083.1 GI:10518157
 KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY of Utah Genome Center
 UNIVERSITY of Utah
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0170 row: P column: 09
 SEQ PRIMER: CACACGAGAACACGCTATGACC
 CLASS: plasmid ends
 HIGH QUALITY sequence stop: 28.
 Location/Qualifiers

JOURNAL COMMENT

1. 28
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0170P09"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g11473211419b/AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

SOURCE

BASE COUNT

0 a 0 c 16 g 12 t

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1152 CCACGACGACCAAAACC 1168
 ||||||||||||||||
 Db 43 CCACGACGACCAAAACC 27

RESULT 10
 AZ315293/c 19 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0032P20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0032P20 F, DNA sequence.
 ACCESSION AZ315293
 VERSION AZ315293.1 GI:10362003
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0032 row: P column: 20
 Seq primer: CTTTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /strain="C57Bl/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0032P20"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57Bl/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g114732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 12 g 7 t
 ORIGIN

Query Match 0.4%; Score 16; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1148 ACACGACGACCA 1163
 ||||||||||||
 Db 18 ACACGACGACCA 3

RESULT 11
 AZ622226/c 20 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0455A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0455A24 R, DNA sequence.
 ACCESSION AZ622226
 VERSION AZ622226.1 GI:11744416
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0455 row: A column: 24
 Seq primer: CACACGAAACGACGATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES
 source
 1..20
 /organism="Mus musculus"
 /strain="C57Bl/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0455A24"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57Bl/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g114732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 14 g 6 t
 ORIGIN

Query Match 0.4%; Score 16; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCACCACCACCACCA 1163
|||||
Db 18 ACCACCACCACCACCA 3

RESULT 12
A2784648 23 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0027P1LR Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0027P1LR R, DNA sequence.
ACCESSION A2784648
VERSION A2784648.1 GI:12920600
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weils,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0027 row: P column: 11
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. 23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0GC2M0027P1L"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1473211419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 2 a 5 c 7 g 9 t
ORIGIN

Query Match 0.4%; Score 16; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3409 ATCCAGTGGAAACAG 3424
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Db 21 ATCCAGTGGAAACAG 6

RESULT 13
A2860972/c 23 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0167A16F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0167A16 F, DNA sequence.
ACCESSION A2860972
VERSION A2860972.1 GI:13056826
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weils,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: A column: 16
Seq primer: CGTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. 23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0GC2M0167A16"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1473211419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 15 g 8 t
ORIGIN

Query Match 0.4%; Score 16; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCAGCAGCACCA 1163
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 Db 21 ACCAGCAGCACCA 6

RESULT 14
 AZ449706 24 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0248M02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0248M02 F, DNA sequence.
 ACCESSION AZ449706
 VERSION AZ449706.1 GI:10603768
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0248 Row: M Column: 02
 Seq Primer: CCGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="UUGC1M0248M02"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
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 adaptor DNA was purified and size-selected for a 9.5 to
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 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g114732114|gb|AF129072.1) a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 7 a 15 c 1 g 1 t
 ORIGIN

Query Match 0.4%; Score 16; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.3e+04;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 ACCAGCAGCACCA 1163
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 Db 5 ACCAGCAGCACCA 20

RESULT 15
 AZ405428 26 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0174D13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0174D13 F, DNA sequence.
 ACCESSION AZ405428
 VERSION AZ405428.1 GI:10529441
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
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 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0174 Row: D Column: 13
 Seq Primer: CCGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 26.
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="UUGC1M0174D13"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
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 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g114732114|gb|AF129072.1) a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 17 g 9 t
 ORIGIN

Query Match 0.4%; Score 16; DB 17; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.3e+04;

Fri Mar 14 14:08:33 2003

us-09-869-894-18.olism50.rst

Page 9

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1148 ACCACCACCACCA 1163

Db 22 ACCACCACCACCA 7

Search completed: March 14, 2003, 08:29:38
Job time : 3697.82 secs

